SEQUENCE LISTING

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C1

<120> Fusion Proteins of Mycobacterium Tuberculosis

<130> 014058-009041US

<140> US 09/688,672
<141> 2000-10-10

<150> US 60/158,338
<151> 1999-10-07

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Asp Phe Val Asn Asn Glu Ala Leu Pro Gly Thr Asp Ile Asp Pro Asp
            20                  25                  30

agc ttc tgg gcg ggc gtc gac aar gtc gtc gcc gac ctg acc ccg cag  144
Ser Phe Trp Ala Gly Val Asp Lys Val Val Ala Asp Leu Thr Pro Gln
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Asn Gln Ala Leu Leu Asn Ala Arg Asp Glu Leu Gln Ala Gln Ile Asp
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aag tgg cac cgg cgt cgg gtg atc gag ccc atc gac atg gat gcc tac  240
Lys Trp His Arg Arg Arg Val Ile Glu Pro Ile Asp Met Asp Ala Tyr
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cgc cag ttc ctc acc gag atc ggc tac ctg ctt ccc gaa cct gat gac  288
Arg Gln Phe Leu Thr Glu Ile Gly Tyr Leu Leu Pro Glu Pro Asp Asp
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ggc ccc cag ctg gtg gtg ccg gtg ctc aac gcg cgg ttt gct ctg aac    384
Gly Pro Gln Leu Val Val Pro Val Leu Asn Ala Arg Phe Ala Leu Asn
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gcg gcc aac gct cgc tgg ggc tcc ctc tac gac gcc ttg tat ggc acc    432
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gat gtc atc ccc gag acc gac ggc gcc gaa aaa ggc ccc acg tac aac    480
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145                 150                 155                 160

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aca gtg cag gat ggc cag ctc gtg gtt gcc ttg ccg gat aag tcc acc    624
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Gly Leu Ala Asn Pro Gly Gln Phe Ala Gly Tyr Thr Gly Ala Ala Glu
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tcg ccg aca tcg gtg ctg cta atc aat cac ggt ttg cac atc gag atc    720
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ctg atc gat ccg gag tcg cag gtc ggc acc acc gac cgg gcc ggc gtc    768
Leu Ile Asp Pro Glu Ser Gln Val Gly Thr Thr Asp Arg Ala Gly Val
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Asp Ser Val Ala Ala Val Asp Ala Ala Asp Lys Val Leu Gly Tyr Arg
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aac tgg ctc ggc ctg aac aag ggc gac ctg gca gca gcg gta gac aag    912
Asn Trp Leu Gly Leu Asn Lys Gly Asp Leu Ala Ala Ala Val Asp Lys
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gac ggc acc gct ttc ctg cgg gtg ctc aat agg gac cgg aac tac acc    960
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gca ccc ggc ggt ggc cag ttc acg ctg cct gga cgc agc ctc atg ttc   1008
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Leu Ile Ala Ile His Gly Leu Lys Ala Ser Asp Val Asn Gly Pro Leu
370 375 380

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Ile Asn Ser Arg Thr Gly Ser Ile Tyr Ile Val Lys Pro Lys Met His
385 390 395 400

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Gly Pro Ala Glu Val Ala Phe Thr Cys Glu Leu Phe Ser Arg Val Glu
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Asp Val Leu Gly Leu Pro Gln Asn Thr Met Lys Ile Gly Ile Met Asp
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Asp Glu Ile His Thr Ser Met Glu Ala Gly Pro Met Val Arg Lys Gly
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acc atg aag agc cag ccg tgg atc ttg gcc tac gag gac cac aac gtc 1488
Thr Met Lys Ser Gln Pro Trp Ile Leu Ala Tyr Glu Asp His Asn Val
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Asp Ala Gly Leu Ala Ala Gly Phe Ser Gly Arg Ala Gln Val Gly Lys
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ggc atg tgg aca atg acc gag ctg atg gcc gac atg gtc gag aca aaa 1584
Gly Met Trp Thr Met Thr Glu Leu Met Ala Asp Met Val Glu Thr Lys
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Ile Ala Gln Pro Arg Ala Gly Ala Ser Thr Ala Trp Val Pro Ser Pro
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gcg gtg caa caa gga ctg gcg ggg aag cgt cgc gcc acc atc gaa caa 1728
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565 570 575

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Ile Arg Glu Glu Val Asp Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val
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gtt cgc tgg gtt gat caa ggt gtc ggc tgc tcg aag gtg ccc gac atc   1872
Val Arg Trp Val Asp Gln Gly Val Gly Cys Ser Lys Val Pro Asp Ile
    610                 615                 620

cac gac gtc gcg ctc atg gag gac cgg gcc acg ctg cga atc tcc agc   1920
His Asp Val Ala Leu Met Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser
625                 630                 635                 640

caa ttg ttg gcc aac tgg ctg cgc cac ggt gtg atc acc agc gcg gat   1968
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gtg cgg gcc agc ttg gag cgg atg gcg ccg ttg gtc gat cga caa aac   2016
Val Arg Ala Ser Leu Glu Arg Met Ala Pro Leu Val Asp Arg Gln Asn
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gcg ggc gac gtg gca tac cga ccg atg gca ccc aac ttc gac gac agt   2064
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Ile Ala Phe Leu Ala Ala Gln Glu Leu Ile Leu Ser Gly Ala Gln Gln
    690                 695                 700

ccc aac ggc tac acc gag ccg atc ctg cac cga cgt cgt cgg gag ttt   2160
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705                 710                 715                 720

aag gcc cgg gcc gct gag aag ccg gcc cca tcg gac agg gcc ggt gac   2208
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Phe Thr Ile Thr Thr Ser Gly Val Asp Ala Glu Ile Thr Thr Thr Ala
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Asp Val Ile Pro Glu Thr Asp Gly Ala Glu Lys Gly Pro Thr Tyr Asn
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195 200 205

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210 215 220

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Asp Gly Thr Ala Phe Leu Arg Val Leu Asn Arg Asp Arg Asn Tyr Thr
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340 345 350

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Gly Met Trp Thr Met Thr Glu Leu Met Ala Asp Met Val Glu Thr Lys
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565 570 575

Leu Leu Thr Ile Pro Leu Ala Lys Glu Leu Ala Trp Ala Pro Asp Glu
580 585 590

Ile Arg Glu Glu Val Asp Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val
595 600 605

Val Arg Trp Val Asp Gln Gly Val Gly Cys Ser Lys Val Pro Asp Ile
610 615 620

His Asp Val Ala Leu Met Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser
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Gln Leu Leu Ala Asn Trp Leu Arg His Gly Val Ile Thr Ser Ala Asp
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Val Arg Ala Ser Leu Glu Arg Met Ala Pro Leu Val Asp Arg Gln Asn
660 665 670

Ala Gly Asp Val Ala Tyr Arg Pro Met Ala Pro Asn Phe Asp Asp Ser
675 680 685

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cgc gtc gcc gaa cgc atc gtc gcc acc aag aag caa ggc aat gac gtc   96
Arg Val Ala Glu Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val
            20                  25                  30

gtc gtc gtc gtc tct gcc atg ggg gat acc acc gac gac ctg ctg gat  144
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ctg gct cag cag gtg tgc ccg gcg ccg ccg cct cgg gag ctg gac atg  192
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ctg ctt acc gcc ggt gaa cgc atc tcg aat gcg ttg gtg gcc atg gcc  240
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65                  70                  75                  80

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Ile Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala
                85                  90                  95

ggg gtg atc acc acc ggc acc cac ggc aac gcc aag atc atc gac gtc  336
Gly Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val
            100                 105                 110

acg ccg ggg cgg ctg caa acc gcc ctt gag gag ggg cgg gtc gtt ttg  384
Thr Pro Gly Arg Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu
        115                 120                 125

gtg gcc gga ttc caa ggg gtc agc cag gac acc aag gat gtc acg acg  432
Val Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr
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ctg ggt gcc gat gtc tgt gag atc tac acc gac gtg gac ggc atc ttc   528
Leu Gly Ala Asp Val Cys Glu Ile Tyr Thr Asp Val Asp Gly Ile Phe
                165                 170                 175

agc gcc gac ccg cgc atc gtg cgc aac gcc cga aag ctc gac acc gtg   576
Ser Ala Asp Pro Arg Ile Val Arg Asn Ala Arg Lys Leu Asp Thr Val
            180                 185                 190

acc ttc gag gaa atg ctc gag atg gcg gcc tgc ggc gcc aag gtg ctg   624
Thr Phe Glu Glu Met Leu Glu Met Ala Ala Cys Gly Ala Lys Val Leu
        195                 200                 205

atg ctg cgc tgc gtg gaa tac gct cgc cgc cat aat att ccg gtg cac   672
Met Leu Arg Cys Val Glu Tyr Ala Arg Arg His Asn Ile Pro Val His
    210                 215                 220

gtc cgg tcg tcg tac tcg gac aga ccg ggc acc gtc gtt gtc gga tcg   720
Val Arg Ser Ser Tyr Ser Asp Arg Pro Gly Thr Val Val Val Gly Ser
225                 230                 235                 240

atc aag gac gta ccc atg gaa gac ccc atc ctg acc gga gtc gcg cac   768
Ile Lys Asp Val Pro Met Glu Asp Pro Ile Leu Thr Gly Val Ala His
                245                 250                 255

gac cgc agc gag gcc aag gtg acc atc gtc ggg ctg ccc gac atc ccc   816
Asp Arg Ser Glu Ala Lys Val Thr Ile Val Gly Leu Pro Asp Ile Pro
            260                 265                 270

ggg tat gcg gcc aag gtg ttt agg gcg gtg gcc aga cgc cga cgt caa   864
Gly Tyr Ala Ala Lys Val Phe Arg Ala Val Ala Arg Arg Arg Arg Gln
        275                 280                 285

cat cga cat ggt gct gca gaa cgt ctc caa ggt cga gga cgg caa gac   912
His Arg His Gly Ala Ala Glu Arg Leu Gln Gly Arg Gly Arg Gln Asp
    290                 295                 300

cga cat cac ctt cac ctg ctc ccg cag acg tcg ggc ccg ccg ccg tgg   960
Arg His His Leu His Leu Leu Pro Gln Thr Ser Gly Pro Pro Pro Trp
305                 310                 315                 320

aaa aac tgg act cgc tca gaa acg aga tcg gct tct aca cag ctg ctg   1008
Lys Asn Trp Thr Arg Ser Glu Thr Arg Ser Ala Ser Thr Gln Leu Leu
                325                 330                 335

tac gac gac cac atc ggc aag gta tcg ctg atc ggt gcc ggc atg cgc   1056
Tyr Asp Asp His Ile Gly Lys Val Ser Leu Ile Gly Ala Gly Met Arg
            340                 345                 350

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Ser His Pro Gly Val Thr Ala Thr Phe Cys Glu Ala Leu Ala Ala Val
        355                 360                 365

ggg gtc aac atc gag ctg atc tcc acc tcg gaa gat cag aga tct cgg   1152
Gly Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Asp Gln Arg Ser Arg
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Cys Cys Ala Ala Thr Pro Asn Trp Thr Arg Pro Trp Ser Arg Cys Met
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aag cgt tcg ggc tcg gcg gcg acg agg agg cca cgg tgt acg cgg gga   1248
Lys Arg Ser Gly Ser Ala Ala Thr Arg Arg Pro Arg Cys Thr Arg Gly
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Val Val Val Val Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp
        35                  40                  45

Leu Ala Gln Gln Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met
    50                  55                  60

Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala
65                  70                  75                  80

Ile Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala
                85                  90                  95

Gly Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val
            100                 105                 110

Thr Pro Gly Arg Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu
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Val Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr
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145                 150                 155                 160

Leu Gly Ala Asp Val Cys Glu Ile Tyr Thr Asp Val Asp Gly Ile Phe
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Ser Ala Asp Pro Arg Ile Val Arg Asn Ala Arg Lys Leu Asp Thr Val
            180                 185                 190

Thr Phe Glu Glu Met Leu Glu Met Ala Ala Cys Gly Ala Lys Val Leu
        195                 200                 205

Met Leu Arg Cys Val Glu Tyr Ala Arg Arg His Asn Ile Pro Val His
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Ile Lys Asp Val Pro Met Glu Asp Pro Ile Leu Thr Gly Val Ala His
245 250 255

Asp Arg Ser Glu Ala Lys Val Thr Ile Val Gly Leu Pro Asp Ile Pro
260 265 270

Gly Tyr Ala Ala Lys Val Phe Arg Ala Val Ala Arg Arg Arg Arg Gln
275 280 285

His Arg His Gly Ala Ala Glu Arg Leu Gln Gly Arg Gly Arg Gln Asp
290 295 300

Arg His His Leu His Leu Leu Pro Gln Thr Ser Gly Pro Pro Pro Trp
305 310 315 320

Lys Asn Trp Thr Arg Ser Glu Thr Arg Ser Ala Ser Thr Gln Leu Leu
325 330 335

Tyr Asp Asp His Ile Gly Lys Val Ser Leu Ile Gly Ala Gly Met Arg
340 345 350

Ser His Pro Gly Val Thr Ala Thr Phe Cys Glu Ala Leu Ala Ala Val
355 360 365

Gly Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Asp Gln Arg Ser Arg
370 375 380

Cys Cys Ala Ala Thr Pro Asn Trp Thr Arg Pro Trp Ser Arg Cys Met
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Pro Arg
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tgacaccttc ttgttcaccc agtacctgtc caagcaagat cccgagggct ggggcaagtc 780
gcccggcttc ggcaccaccg tcgacttccc ggcggtgccg ggtgcgctgg gtgagaacgg 840
caacggcggc atggtgaccg gttgcgccga gacaccgggc tgcgtggcct atatcggcat 900
cagcttcctc gaccaggcca gtcaacgggg actcggcgag gcccaactag gcaatagctc 960
tggcaatttc ttgttgcccg acgcgcaaag cattcaggcc gcggcggctg gcttcgcatc 1020
gaaaaccccg gcgaaccagg cgatttcgat gatcgacggg cccgccccgg acggctaccc 1080
gatcatcaac tacgagtacg ccatcgtcaa caaccggcaa aaggacgccg ccaccgcgca 1140
gaccttgcag gcatttctgc actgggcgat caccgacggc aacaaggcct cgttcctcga 1200
ccaggttcat ttccagccgc tgccgcccgc ggtggtgaag ttgtctgacg cgttgatcgc 1260
gacgatttcc agctagcctc gttgaccacc acgcgacagc aacctccgtc gggccatcgg 1320
gctgctttgc ggagcatgct ggcccgtgcc ggtgaagtcg gccgcgctgg cccggccatc 1380
cggtggttgg gtgggatagg tgcggtgatc ccgctgcttg cgctggtctt ggtgctggtg 1440
gtgctggtca tcgaggcgat gggtgcgatc aggctcaacg ggttgcattt cttcaccgcc 1500
accgaatgga atccaggcaa cacctacggc gaaaccgttg tcaccgacgc gtcgcccatc 1560
cggtcggcgc ctactacggg gcgttgccgc tgatcgtcgg gacgctggcg acctcggcaa 1620

tcgccctgat catcgcggtg ccggtctctg taggagcggc gctggtgatc gtggaacggc 1680
tgccgaaacg gttggccgag gctgtgggaa tagtcctgga attgctcgcc ggaatcccca 1740
gcgtggtcgt cggtttgtgg ggggcaatga cgttcgggcc gttcatcgct catcacatcg 1800
ctccggtgat cgctcacaac gctcccgatg tgccggtgct gaactacttg cgcggcgacc 1860
cgggcaacgg ggagggcatg ttggtgtccg gtctggtgtt ggcggtgatg gtcgttccca 1920
ttatcgccac caccactcat gacctgttcc ggcaggtgcc ggtgttgccc cgggagggcg 1980
cgatcgggaa ttc 1993

<210> 8
<211> 374
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> 38kD

<400> 8
Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
1 5 10 15

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
20 25 30

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
35 40 45

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
50 55 60

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
65 70 75 80

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
85 90 95

Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
100 105 110

Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
115 120 125

Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
130 135 140

Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
145 150 155 160

Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
165 170 175

Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
180 185 190

Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
195 200 205

Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
210 215 220

```
Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
225                 230                 235                 240

Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
                245                 250                 255

Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
            260                 265                 270

Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe
        275                 280                 285

Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
    290                 295                 300

Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
305                 310                 315                 320

Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
                325                 330                 335

His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
            340                 345                 350

His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
        355                 360                 365

Ile Ala Thr Ile Ser Ser
    370
```

<210> 9
<211> 327
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb11 (Tb38-1)

<400> 9
```
cggcacgaga gaccgatgcc gctaccctcg cgcaggaggc aggtaatttc gagcggatct 60
ccggcgacct gaaaacccag atcgaccagg tggagtcgac ggcaggttcg ttgcagggcc 120
agtggcgcgg cgcggcgggg acggccgccc aggccgcggt ggtgcgcttc caagaagcag 180
ccaataagca gaagcaggaa ctcgacgaga tctcgacgaa tattcgtcag gccggcgtcc 240
aatactcgag ggccgacgag gagcagcagc aggcgctgtc ctcgcaaatg ggcttctgac 300
ccgctaatac gaaaagaaac ggagcaa                                     327
```

<210> 10
<211> 95
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb11 (Tb38-1)

<400> 10
```
Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
  1               5                  10                  15
```

Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
20 25 30

Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
35 40 45

Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
50 55 60

Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
65 70 75 80

Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
85 90 95

<210> 11
<211> 702
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> TbH4

<220>
<221> modified_base
<222> (1)..(702)
<223> n = g, a, c or t

<400> 11
cggcacgagg atcggtaccc cgcggcatcg gcagctgccg attcgccggg tttccccacc 60
cgaggaaagc cgctaccaga tggcgctgcc gaagtagggc gatccgttcg cgatgccggc 120
atgaacgggc ggcatcaaat tagtgcagga acctttcagt ttagcgacga taatggctat 180
agcactaagg aggatgatcc gatatgacgc agtcgcagac cgtgacggtg gatcagcaag 240
agattttgaa cagggccaac gaggtggagg ccccgatggc ggacccaccg actgatgtcc 300
ccatcacacc gtgcgaactc acggnggnta aaaacgccgc ccaacagntg gtnttgtccg 360
ccgacaacat gcgggaatac ctggcggccg gtgccaaaga gcggcagcgt ctggcgacct 420
cgctgcgcaa cgcggccaag gngtatggcg aggttgatga ggaggctgcg accgcgctgg 480
acaacgacgg cgaaggaact gtgcaggcag aatcggccgg ggccgtcgga ggggacagtt 540
cggccgaact aaccgatacg ccgagggtgg ccacggccgg tgaacccaac ttcatggatc 600
tcaaagaagc ggcaaggaag ctcgaaacgg gcgaccaagg cgcatcgctc gcgcactgng 660
gggatgggtg gaacacttnc accctgacgc tgcaaggcga cg 702

<210> 12
<211> 286
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> TbH4

<220>
<221> MOD_RES
<222> (1)..(286)
<223> Xaa = any amino acid

<400> 12
Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
1 5 10 15

Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
20 25 30

His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
35 40 45

Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
50 55 60

Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
65 70 75 80

Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
85 90 95

Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
100 105 110

Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
115 120 125

Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
130 135 140

Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
145 150 155 160

Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
165 170 175

Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
180 185 190

Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
195 200 205

Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
210 215 220

Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
225 230 235 240

Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
245 250 255

Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
260 265 270

Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
275 280 285

<210> 13
<211> 1200
<212> DNA
<213> Mycobacterium tuberculosis

<400> 13
caggcatgag cagagcgttc atcatcgatc caacgatcag tgccattgac ggcttgtacg 60
accttctggg gattggaata cccaaccaag ggggtatcct ttactcctca ctagagtact 120
tcgaaaaagc cctggaggag ctggcagcag cgtttccggg tgatggctgg ttaggttcgg 180

ccgcggacaa atacgccggc aaaaaccgca accacgtgaa ttttttccag gaactggcag 240
acctcgatcg tcagctcatc agcctgatcc acgaccaggc caacgcggtc cagacgaccc 300
gcgacatcct ggagggcgcc aagaaaggtc tcgagttcgt gcgcccggtg gctgtggacc 360
tgacctacat cccggtcgtc gggcacgccc tatcggccgc cttccaggcg ccgttttgcg 420
cgggcgcgat ggccgtagtg ggcggcgcgc ttgcctactt ggtcgtgaaa acgctgatca 480
acgcgactca actcctcaaa ttgcttgcca aattggcgga gttggtcgcg gccgccattg 540
cggacatcat ttcggatgtg gcggacatca tcaagggcac cctcggagaa gtgtgggagt 600
tcatcacaaa cgcgctcaac ggcctgaaag agctttggga caagctcacg gggtgggtga 660
ccggactgtt ctctcgaggg tggtcgaacc tggagtcctt ctttgcgggc gtccccggct 720
tgaccggcgc gaccagcggc ttgtcgcaag tgactggctt gttcggtgcg gccggtctgt 780
ccgcatcgtc gggcttggct cacgcggata gcctggcgag ctcagccagc ttgcccgccc 840
tggccggcat tgggggcggg tccggttttg ggggcttgcc gagcctggct caggtccatg 900
ccgcctcaac tcggcaggcg ctacggcccc gagctgatgg cccggtcggc gccgctgccg 960
agcaggtcgg cgggcagtcg cagctggtct ccgcgcaggg ttcccaaggt atgggcggac 1020
ccgtaggcat gggcggcatg cacccctctt cgggggcgtc gaaagggacg acgacgaaga 1080
agtactcgga aggcgcggcg gcgggcactg aagacgccga gcgcgcgcca gtcgaagctg 1140
acgcgggcgg tgggcaaaag gtgctggtac gaaacgtcgt ctaacggcat ggcgagccaa 1200

<210> 14
<211> 392
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> HTCC#1 (Mtb40)

<400> 14
Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15

Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20 25 30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35 40 45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50 55 60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65 70 75 80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85 90 95

Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
100 105 110

Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
115 120 125

Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
130 135 140

Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145 150 155 160

Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165 170 175

```
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
            180                 185                 190

Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
        195                 200                 205

Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
    210                 215                 220

Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225                 230                 235                 240

Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
                245                 250                 255

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
            260                 265                 270

Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
        275                 280                 285

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
    290                 295                 300

Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
305                 310                 315                 320

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
                325                 330                 335

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
            340                 345                 350

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
        355                 360                 365

Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
    370                 375                 380

Lys Val Leu Val Arg Asn Val Val
385                 390
```

<210> 15
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 (1-232)

<220>
<221> CDS
<222> (1)..(720)

<400> 15

```
atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat cca   48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
  1               5                  10                  15
```

```
acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata    96
Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
             20                  25                  30

ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa   144
Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
         35                  40                  45

gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt   192
Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
     50                  55                  60

tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt   240
Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
 65                  70                  75                  80

ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac   288
Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
                 85                  90                  95

gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc   336
Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
            100                 105                 110

aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac   384
Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
        115                 120                 125

atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg ttt   432
Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
    130                 135                 140

tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt gcc tac ttg gtc   480
Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val
145                 150                 155                 160

gtg aaa acg ctg atc aac gcg act caa ctc ctc aaa ttg ctt gcc aaa   528
Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys
                165                 170                 175

ttg gcg gag ttg gtc gcg gcc gcc att gcg gac atc att tcg gat gtg   576
Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
            180                 185                 190

gcg gac atc atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc aca   624
Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr
        195                 200                 205

aac gcg ctc aac ggc ctg aaa gag ctt tgg gac aag ctc acg ggg tgg   672
Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp
    210                 215                 220

gtg acc gga ctg ttc tct cga ggg tgg tcg aac ctg gag tcc ttc taa   720
Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe
225                 230                 235                 240

gaattc                                                           726
```

<210> 16
<211> 239
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:HTCC#1 (1-232)

<400> 16
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
1 5 10 15

Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
20 25 30

Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
35 40 45

Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
50 55 60

Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
65 70 75 80

Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
85 90 95

Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
100 105 110

Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
115 120 125

Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
130 135 140

Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val
145 150 155 160

Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys
165 170 175

Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
180 185 190

Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr
195 200 205

Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp
210 215 220

Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe
225 230 235

<210> 17
<211> 661
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1
(184-392)

<220>
<221> CDS
<222> (1)..(651)

<400> 17

```
atg cat cac cat cac cat cac gat gtg gcg gac atc atc aag ggc atc   48
Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Ile
  1               5                  10                  15

ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa   96
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
             20                  25                  30

gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga  144
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
         35                  40                  45

ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc  192
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
     50                  55                  60

ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc  240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
 65                  70                  75                  80

ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc  288
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
                 85                  90                  95

tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt  336
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
            100                 105                 110

ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg cag  384
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
        115                 120                 125

gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag  432
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
    130                 135                 140

gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg  480
Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
145                 150                 155                 160

ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg  528
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
                165                 170                 175

aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act  576
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
            180                 185                 190

gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa  624
Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
        195                 200                 205

aag gtg ctg gta cga aac gtc gtc taa cggcgaattc                  661
Lys Val Leu Val Arg Asn Val Val
    210                 215
```

<210> 18
<211> 216
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:HTCC#1
(184-392)

<400> 18
Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Ile
1 5 10 15

Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
20 25 30

Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
35 40 45

Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
50 55 60

Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
65 70 75 80

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
85 90 95

Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
100 105 110

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
115 120 125

Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
130 135 140

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
145 150 155 160

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
165 170 175

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
180 185 190

Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
195 200 205

Lys Val Leu Val Arg Asn Val Val
210 215

<210> 19
<211> 411
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 (1-129)

<220>
<221> CDS
<222> (1)..(411)

<400> 19
atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat cca 48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
1 5 10 15

acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata 96
Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
20 25 30

ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa 144
Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
35 40 45

gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt 192
Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
50 55 60

tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt 240
Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
65 70 75 80

ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac 288
Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
85 90 95

gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc 336
Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
100 105 110

aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac 384
Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
115 120 125

atc ccg gtc gtc ggg cac gcc cta tag 411
Ile Pro Val Val Gly His Ala Leu
130 135

<210> 20
<211> 136
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:HTCC#1 (1-129)

<400> 20
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
1 5 10 15

Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
20 25 30

Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
35 40 45

Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
50 55 60

```
Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
 65                  70                  75                  80

Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
                85                  90                  95

Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
            100                 105                 110

Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
        115                 120                 125

Ile Pro Val Val Gly His Ala Leu
    130                 135
```

<210> 21
<211> 1225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 (TM-1)

<220>
<221> CDS
<222> (4)..(1215)

<400> 21

```
cat atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat   48
    Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp
      1               5                  10                  15

cca acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga   96
Pro Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly
                20                  25                  30

ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa  144
Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu
            35                  40                  45

aaa gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta  192
Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu
        50                  55                  60

ggt tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat  240
Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn
    65                  70                  75

ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc  288
Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile
80                  85                  90                  95

cac gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc  336
His Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly
                100                 105                 110

gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc  384
Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr
            115                 120                 125
```

```
tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg   432
Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro
        130                 135                 140

ttt tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt aag ctt gcc   480
Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Ala
    145                 150                 155

tac ttg gtc gtg aaa acg ctg atc aac gcg aag ctt act caa ctc ctc   528
Tyr Leu Val Val Lys Thr Leu Ile Asn Ala Lys Leu Thr Gln Leu Leu
160                 165                 170                 175

aaa ttg ctt gcc aaa ttg gcg gag ttg gtc gcg gcc gcc att gcg gac   576
Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp
                180                 185                 190

atc att tcg gat gtg gcg gac atc atc aag ggc atc ctc gga gaa gtg   624
Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val
            195                 200                 205

tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa gag ctt tgg gac   672
Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp
        210                 215                 220

aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga ggg tgg tcg aac   720
Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn
    225                 230                 235

ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc ggc gcg acc agc   768
Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser
240                 245                 250                 255

ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca   816
Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala
                260                 265                 270

tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc tca gcc agc ttg   864
Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu
            275                 280                 285

ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt ggg ggc ttg ccg   912
Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro
        290                 295                 300

agc ctg gct cag gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc   960
Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro
    305                 310                 315

cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag gtc ggc ggg cag  1008
Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln
320                 325                 330                 335

tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta  1056
Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val
                340                 345                 350

ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg  1104
Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr
            355                 360                 365
```

```
acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag   1152
Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu
        370                 375                 380

cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta   1200
Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val
    385                 390                 395

cga aac gtc gtc taa cggcgaattc
Arg Asn Val Val                                                   1225
400
```

<210> 22
<211> 403
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:HTCC#1 (TM-1)

<400> 22

```
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
  1               5                  10                  15

Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
            20                  25                  30

Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
        35                  40                  45

Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
    50                  55                  60

Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
65                  70                  75                  80

Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
                85                  90                  95

Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
            100                 105                 110

Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
        115                 120                 125

Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
    130                 135                 140

Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Ala Tyr
145                 150                 155                 160

Leu Val Val Lys Thr Leu Ile Asn Ala Lys Leu Thr Gln Leu Leu Lys
                165                 170                 175

Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile
            180                 185                 190

Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp
        195                 200                 205

Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys
    210                 215                 220
```

Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu
225 230 235 240

Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly
245 250 255

Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser
260 265 270

Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro
275 280 285

Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser
290 295 300

Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg
305 310 315 320

Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser
325 330 335

Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
340 345 350

Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr
355 360 365

Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg
370 375 380

Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg
385 390 395 400

Asn Val Val

<210> 23
<211> 1225
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 (TM-2)

<220>
<221> CDS
<222> (4)..(1215)

<400> 23
cat atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat 48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp
1 5 10 15

cca acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga 96
Pro Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly
20 25 30

ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa 144
Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu
35 40 45

```
aaa gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta   192
Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu
          50                  55                  60

ggt tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat   240
Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn
      65                  70                  75

ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc   288
Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile
 80                  85                  90                  95

cac gac cag gcc aac gcg gtc cag acg acc cgc gac aag ctt atc ctg   336
His Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Lys Leu Ile Leu
                100                 105                 110

gag ggc gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac   384
Glu Gly Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp
            115                 120                 125

ctg acc tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag   432
Leu Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln
        130                 135                 140

gcg ccg ttt tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt gcc   480
Ala Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala
    145                 150                 155

tac ttg gtc gtg aaa acg ctg atc aac gcg act caa ctc ctc aaa ttg   528
Tyr Leu Val Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu
160                 165                 170                 175

ctt gcc aaa ttg gcg gag ttg gtc gcg gcc gcc att gcg gac atc att   576
Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile
                180                 185                 190

tcg gat gtg gcg gac atc atc aag ggc atc ctc gga gaa gtg tgg gag   624
Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu
            195                 200                 205

ttc atc aca aac gcg aag ctt ctc aac ggc ctg aaa gag ctt tgg gac   672
Phe Ile Thr Asn Ala Lys Leu Leu Asn Gly Leu Lys Glu Leu Trp Asp
        210                 215                 220

aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga ggg tgg tcg aac   720
Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn
    225                 230                 235

ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc ggc gcg acc agc   768
Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser
240                 245                 250                 255

ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca   816
Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala
                260                 265                 270

tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc tca gcc agc ttg   864
Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu
            275                 280                 285
```

```
ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt ggg ggc ttg ccg   912
Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro
        290                 295                 300

agc ctg gct cag gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc   960
Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro
    305                 310                 315

cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag gtc ggc ggg cag   1008
Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln
320                 325                 330                 335

tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta   1056
Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val
                340                 345                 350

ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg   1104
Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr
            355                 360                 365

acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag   1152
Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu
        370                 375                 380

cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta   1200
Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val
    385                 390                 395

cga aac gtc gtc taa cggcgaattc                                   1225
Arg Asn Val Val
400
```

<210> 24
<211> 403
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:HTCC#1 (TM-2)

<400> 24

```
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
  1               5                  10                  15

Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
            20                  25                  30

Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
        35                  40                  45

Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
    50                  55                  60

Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
65                  70                  75                  80

Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
                85                  90                  95

Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Lys Leu Ile Leu Glu
            100                 105                 110
```

Gly Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu
115 120 125

Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala
130 135 140

Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr
145 150 155 160

Leu Val Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu
165 170 175

Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser
180 185 190

Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe
195 200 205

Ile Thr Asn Ala Lys Leu Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys
210 215 220

Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu
225 230 235 240

Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly
245 250 255

Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser
260 265 270

Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro
275 280 285

Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser
290 295 300

Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg
305 310 315 320

Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser
325 330 335

Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
340 345 350

Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr
355 360 365

Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg
370 375 380

Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg
385 390 395 400

Asn Val Val

<210> 25
<211> 3058
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> TbH9 (Mtb39A)

<400> 25
gatcgtaccc gtgcgagtgc tcgggccgtt tgaggatgga gtgcacgtgt ctttcgtgat 60
ggcataccca gagatgttgg cggcggcggc tgacaccctg cagagcatcg gtgctaccac 120
tgtggctagc aatgccgctg cggcggcccc gacgactggg gtggtgcccc ccgctgccga 180
tgaggtgtcg gcgctgactg cggcgcactt cgccgcacat gcggcgatgt atcagtccgt 240
gagcgctcgg gctgctgcga ttcatgacca gttcgtggcc acccttgcca gcagcgccag 300
ctcgtatgcg gccactgaag tcgccaatgc ggcggcggcc agctaagcca ggaacagtcg 360
gcacgagaaa ccacgagaaa tagggacacg taatggtgga tttcggggcg ttaccaccgg 420
agatcaactc cgcgaggatg tacgccggcc cgggttcggc ctcgctggtg gccgcggctc 480
agatgtggga cagcgtggcg agtgacctgt tttcggccgc gtcggcgttt cagtcggtgg 540
tctggggtct gacggtgggg tcgtggatag gttcgtcggc gggtctgatg gtggcggcgg 600
cctcgccgta tgtggcgtgg atgagcgtca ccgcggggca ggccgagctg accgccgccc 660
aggtccgggt tgctgcggcg gcctacgaga cggcgtatgg gctgacggtg cccccgccgg 720
tgatcgccga gaaccgtgct gaactgatga ttctgatagc gaccaacctc ttggggcaaa 780
acaccccggc gatcgcggtc aacgaggccg aatacggcga gatgtgggcc caagacgccg 840
ccgcgatgtt tggctacgcc gcggcgacgg cgacggcgac ggcgacgttg ctgccgttcg 900
aggaggcgcc ggagatgacc agcgcgggtg ggctcctcga gcaggccgcc gcggtcgagg 960
aggcctccga caccgccgcg gcgaaccagt tgatgaacaa tgtgccccag gcgctgcaac 1020
agctggccca gcccacgcag ggcaccacgc cttcttccaa gctgggtggc ctgtggaaga 1080
cggtctcgcc gcatcggtcg ccgatcagca acatggtgtc gatggccaac aaccacatgt 1140
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ctccggcggc ggccgcccag gccgtgcaaa ccgcggcgca aaacggggtc cgggcgatga 1260
gctcgctggg cagctcgctg ggttcttcgg gtctgggcgg tggggtggcc gccaacttgg 1320
gtcgggcggc ctcggtcggt tcgttgtcgg tgccgcaggc ctgggccgcg gccaaccagg 1380
cagtcacccc ggcggcgcgg gcgctgccgc tgaccagcct gaccagcgcc gcggaaagag 1440
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ggctcagtgg tgtgctgcgt gttccgccgc gaccctatgt gatgccgcat tctccggcgg 1560
ccggctagga gaggggcgc agactgtcgt tatttgacca gtgatcggcg gtctcggtgt 1620
ttccgcggcc ggctatgaca acagtcaatg tgcatgacaa gttacaggta ttaggtccag 1680
gttcaacaag gagacaggca acatggcctc acgttttatg acggatccgc acgcgatgcg 1740
ggacatggcg ggccgttttg aggtgcacgc ccagacggtg gaggacgagg ctcgccggat 1800
gtgggcgtcc gcgcaaaaca tttccggtgc gggctggagt ggcatggccg aggcgacctc 1860
gctagacacc atggcccaga tgaatcaggc gtttcgcaac atcgtgaaca tgctgcacgg 1920
ggtgcgtgac gggctggttc gcgacgccaa caactacgag cagcaagagc aggcctccca 1980
gcagatcctc agcagctaac gtcagccgct gcagcacaat acttttacaa gcgaaggaga 2040
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cgcgctcagg ccgggttgct ggaggccgag catcaggcca tcattcgtga tgtgttgacc 2160
gcgagtgact tttggggcgg cgccggttcg gcggcctgcc aggggttcat tacccagttg 2220
ggccgtaact tccaggtgat ctacgagcag gccaacgccc acgggcagaa ggtgcaggct 2280
gccggcaaca acatggcgca aaccgacagc gccgtcggct ccagctgggc ctgacaccag 2340
gccaaggcca gggacgtggt gtacgagtga agttcctcgc gtgatccttc gggtggcagt 2400
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cagtgctgct cgggctcggg tgaggacctc gaggcccagg tagcgccgtc cttcgatcca 2520
ttcgtcgtgt tgttcggcga ggacggctcc gacgaggcgg atgatcgagg cgcggtcggg 2580
gaagatgccc acgacgtcgg ttcggcgtcg tacctctcgg ttgaggcgtt cctgggggtt 2640
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gcgggcggtg tcgaggtgct cggccaccgc ggggagtttg tcggtcagag cgtcgagtac 2760
ccgatcatat tgggcaacaa ctgattcggc gtcgggctgg tcgtagatgg agtgcagcag 2820
ggtgcgcacc cacggccagg agggcttcgg ggtggctgcc atcagattgg ctgcgtagtg 2880
ggttctgcag cgctgccagg ccgctgcggg cagggtggcg ccgatcgcgg ccaccaggcc 2940
ggcgtgggcg tcgctggtga ccagcgcgac cccggacagg ccgcgggcga ccaggtcgcg 3000
gaagaacgcc agccagccgg ccccgtcctc ggcggaggtg acctggatgc ccaggatc 3058

<210> 26
<211> 391
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> TbH9 (Mtb39A)

<400> 26

```
Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1               5                  10                  15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
            20                  25                  30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
        35                  40                  45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
    50                  55                  60

Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
65                  70                  75                  80

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
                85                  90                  95

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
            100                 105                 110

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
        115                 120                 125

Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
    130                 135                 140

Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
145                 150                 155                 160

Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
                165                 170                 175

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
            180                 185                 190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
        195                 200                 205

Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
    210                 215                 220

Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
225                 230                 235                 240

Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
                245                 250                 255

Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
            260                 265                 270

Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
        275                 280                 285

Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
    290                 295                 300
```

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
305 310 315 320

Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
325 330 335

Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
340 345 350

Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
355 360 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
370 375 380

Pro His Ser Pro Ala Ala Gly
385 390

<210> 27
<211> 447
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> TbRa12

<400> 27
cggtatgaac acggccgcgt ccgataactt ccagctgtcc cagggtgggc agggattcgc 60
cattccgatc gggcaggcga tggcgatcgc gggccagatc cgatcgggtg gggggtcacc 120
caccgttcat atcgggccta ccgccttcct cggcttgggt gttgtcgaca acaacggcaa 180
cggcgcacga gtccaacgcg tggtcgggag cgctccggcg gcaagtctcg gcatctccac 240
cggcgacgtg atcaccgcgg tcgacggcgc tccgatcaac tcggccaccg cgatggcgga 300
cgcgcttaac gggcatcatc ccggtgacgt catctcggtg aactggcaaa ccaagtcggg 360
cggcacgcgt acagggaacg tgacattggc cgagggaccc ccggcctgat ttcgtcgygg 420
ataccacccg ccggccggcc aattgga 447

<210> 28
<211> 132
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> TbRa12

<400> 28
Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15

Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20 25 30

Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35 40 45

Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50 55 60

Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65 70 75 80

Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85 90 95

Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100 105 110

Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115 120 125

Gly Pro Pro Ala
130

<210> 29
<211> 1872
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> TbRa35 (Mtb32A)

<400> 29
gactacgttg gtgtagaaaa atcctgccgc ccggaccctt aaggctggga caatttctga 60
tagctacccc gacacaggag gttacgggat gagcaattcg cgccgccgct cactcaggtg 120
gtcatggttg ctgagcgtgc tggctgccgt cgggctgggc ctggccacgg cgccggccca 180
ggcggccccg ccggccttgt cgcaggaccg gttcgccgac ttccccgcgc tgcccctcga 240
cccgtccgcg atggtcgccc aagtggcgcc acaggtggtc aacatcaaca ccaaactggg 300
ctacaacaac gccgtgggcg ccgggaccgg catcgtcatc gatcccaacg gtgtcgtgct 360
gaccaacaac cacgtgatcg cgggcgccac cgacatcaat gcgttcagcg tcggctccgg 420
ccaaacctac ggcgtcgatg tggtcgggta tgaccgcacc caggatgtcg cggtgctgca 480
gctgcgcggt gccggtggcc tgccgtcggc ggcgatcggt ggcggcgtcg cggttggtga 540
gcccgtcgtc gcgatgggca acagcggtgg gcagggcgga acgccccgtg cggtgcctgg 600
cagggtggtc gcgctcggcc aaaccgtgca ggcgtcggat tcgctgaccg gtgccgaaga 660
gacattgaac gggttgatcc agttcgatgc cgcaatccag cccggtgatt cgggcgggcc 720
cgtcgtcaac ggcctaggac aggtggtcgg tatgaacacg gccgcgtccg ataacttcca 780
gctgtcccag ggtgggcagg gattcgccat tccgatcggg caggcgatgg cgatcgcggg 840
ccaaatccga tcgggtgggg ggtcacccac cgttcatatc gggcctaccg ccttcctcgg 900
cttgggtgtt gtcgacaaca acggcaacgg cgcacgagtc caacgcgtgg tcggaagcgc 960
tccggcggca agtctcggca tctccaccgg cgacgtgatc accgcggtcg acggcgctcc 1020
gatcaactcg gccaccgcga tggcggacgc gcttaacggg catcatcccg gtgacgtcat 1080
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cagccgtgat tgccgcgtga gcccccgagt tccgtctccc gtgcgcgtgg cattgtggaa 1260
gcaatgaacg aggcagaaca cagcgttgag cacccctccg tgcagggcag ttacgtcgaa 1320
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gatccgacct ggtttaagca cgccgtcttc tacgaggtgc tggtccgggc gttcttcgac 1440
gccagcgcgg acggttccgn cgatctgcgt ggactcatcg atcgcctcga ctacctgcag 1500
tggcttggca tcgactgcat ctgttgccgc cgttcctacg actcaccgct gcgcgacggc 1560
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aatcacacct cggagtcgca cccctggttt caggagtccc gccgcgaccc agacggaccg 1740
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ttcgtcgaca ccgaagagtc gaactggtca ttcgatcctg tccgccgaca gttnctactg 1860
gcaccgattc tt 1872

<210> 30
<211> 355
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> TbRa35 (Mtb32A)

<400> 30

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Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
  1               5                  10                  15

Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
            20                  25                  30

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
        35                  40                  45

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
    50                  55                  60

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
65                  70                  75                  80

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
                85                  90                  95

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
            100                 105                 110

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
        115                 120                 125

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
    130                 135                 140

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
145                 150                 155                 160

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
                165                 170                 175

Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
            180                 185                 190

Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
        195                 200                 205

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
    210                 215                 220

Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
225                 230                 235                 240

Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
                245                 250                 255

Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
            260                 265                 270

Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
        275                 280                 285

Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
    290                 295                 300
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Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
305 310 315 320

Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
325 330 335

Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
340 345 350

Pro Pro Ala
355

<210> 31
<211> 1441
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> MTCC#2 (Mtb41)

<400> 31
gaggttgctg gcaatggatt tcgggctttt acctccggaa gtgaattcaa gccgaatgta 60
ttccggtccg gggccggagt cgatgctagc cgccgcggcc gcctgggacg gtgtggccgc 120
ggagttgact tccgccgcgg tctcgtatgg atcggtggtg tcgacgctga tcgttgagcc 180
gtggatgggg ccggcggcgg ccgcgatggc ggccgcggca acgccgtatg tggggtggct 240
ggccgccacg gcggcgctgg cgaaggagac ggccacacag gcgagggcag cggcggaagc 300
gtttgggacg gcgttcgcga tgacggtgcc accatccctc gtcgcggcca accgcagccg 360
gttgatgtcg ctggtcgcgg cgaacattct ggggcaaaac agtgcggcga tcgcggctac 420
ccaggccgag tatgccgaaa tgtgggccca agacgctgcc gtgatgtaca gctatgaggg 480
ggcatctgcg gccgcgtcgg cgttgccgcc gttcactcca cccgtgcaag gcaccggccc 540
ggccgggccc gcggccgcag ccgcggcgac ccaagccgcc ggtgcgggcg ccgttgcgga 600
tgcacaggcg acactggccc agctgccccc ggggatcctg agcgacattc tgtccgcatt 660
ggccgccaac gctgatccgc tgacatcggg actgttgggg atcgcgtcga ccctcaaccc 720
gcaagtcgga tccgctcagc cgatagtgat ccccaccccg ataggggaat tggacgtgat 780
cgcgctctac attgcatcca tcgcgaccgg cagcattgcg ctcgcgatca cgaacacggc 840
cagaccctgg cacatcggcc tatacgggaa cgccggcggg ctgggaccga cgcagggcca 900
tccactgagt tcggcgaccg acgagccgga gccgcactgg ggccccttcg ggggcgcggc 960
gccggtgtcc gcgggcgtcg gccacgcagc attagtcgga gcgttgtcgg tgccgcacag 1020
ctggaccacg gccgccccgg agatccagct cgccgttcag gcaacaccca ccttcagctc 1080
cagcgccggc gccgacccga cggccctaaa cgggatgccg gcaggcctgc tcagcgggat 1140
ggctttggcg agcctggccg cacgcggcac gacgggcggt ggcggcaccc gtagcggcac 1200
cagcactgac ggccaagagg acggccgcaa acccccggta gttgtgatta gagagcagcc 1260
gccgcccgga aacccccccgc ggtaaaagtc cggcaaccgt tcgtcgccgc gcggaaaatg 1320
cctggtgagc gtggctatcc gacgggccgt tcacaccgct tgtagtagcg tacggctatg 1380
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g 1441

<210> 32
<211> 423
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> MTTC#2 (Mtb41)

<400> 32
Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
1 5 10 15

Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp
20 25 30

Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
35 40 45

Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
50 55 60

Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
65 70 75 80

Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
85 90 95

Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
100 105 110

Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
115 120 125

Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
130 135 140

Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
145 150 155 160

Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
165 170 175

Ala Gly Pro Ala Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
180 185 190

Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
195 200 205

Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
210 215 220

Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
225 230 235 240

Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
245 250 255

Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
260 265 270

Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
275 280 285

Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
290 295 300

Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
305 310 315 320

Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
325 330 335

Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
340 345 350

Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
355 360 365

Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
370 375 380

Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
385 390 395 400

Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
405 410 415

Pro Pro Gly Asn Pro Pro Arg
420

<210> 33
<211> 1742
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.9A (MTI-A)

<220>
<221> modified_base
<222> (1)..(1742)
<223> n = g, a, c or t

<400> 33
ccgctctctt tcaacgtcat aagttcggtg ggccagtcgg ccgcgcgtgc atatggcacc 60
aataacgcgt gtcccatgga tacccggacc gcacgacggt agagcggatc agcgcagccg 120
gtgccgaaca ctaccgcgtc cacgctcagc cctgccgcgt tgcggaagat cgagcccagg 180
ttctcatggt cgttaacgcc ttccaacact gcgacggtgc gcgccccggc gaccacctga 240
gcaacgctcg gctccggcac ccggcgcgcg gctgccaaca ccccacgatt gagatggaag 300
ccgatcaccc gtgccatgac atcagccgac gctcgatagt acggcgcgcc gacaccggcc 360
agatcatcct tgagctcggc cagccggcgg tcggtgccga acagcgccag cggcgtgaac 420
cgtgaggcca gcatgcgctg caccaccagc acaccctcgg cgatcaccaa cgccttgccg 480
gtcggcagat cgggacnacn gtcgatgctg ttcaggtcac ggaaatcgtc gagccgtggg 540
tcgtcgggat cgcagacgtc ctgaacatcg aggccgtcgg ggtgctgggc acaacggcct 600
tcggtcacgg gctttcgtcg accagagcca gcatcagatc ggcggcgctg cgcaggatgt 660
cacgctcgct gcggttcagc gtcgcgagcc gctcagccag ccactcttgc agagagccgt 720
tgctgggatt aattgggaga ggaagacagc atgtcgttcg tgaccacaca gccggaagcc 780
ctggcagctg cggcggcgaa cctacagggt attggcacga caatgaacgc ccagaacgcg 840
gccgcggctg ctccaaccac cggagtagtg cccgcagccg ccgatgaagt atcagcgctg 900
accgcggctc agtttgctgc gcacgcgcag atgtaccaaa cggtcagcgc ccaggccgcg 960
gccattcacg aaatgttcgt gaacacgctg gtggccagtt ctggctcata cgcggccacc 1020
gaggcggcca acgcagccgc tgccggctga acgggctcgc acgaacctgc tgaaggagag 1080
ggggaacatc cggagttctc gggtcagggg ttgcgccagc gcccagccga ttcagntatc 1140
ggcgtccata acagcagacg atctaggcat tcagtactaa ggagacaggc aacatggcct 1200
cacgttttat gacggatccg catgcgatgc gggacatggc gggccgtttt gaggtgcacg 1260
cccagacggt ggaggacgag gctcgccgga tgtgggcgtc cgcgcaaaac atttccggtg 1320
cgggctggag tggcatggcc gaggcgacct cgctagacac catgacctag atgaatcagg 1380
cgtttcgcaa catcgtgaac atgctgcacg gggtgcgtga cgggctggtt cgcgacgcca 1440
acaantacga acagcaagag caggcctccc agcagatcct gagcagntag cgccgaaagc 1500
cacagctgng tacgntttct cacattagga gaacaccaat atgacgatta attaccagtt 1560
cggggacgtc gacgctcatg gcgccatgat ccgcgctcag gcggcgtcgc ttgaggcgga 1620
gcatcaggcc atcgttcgtg atgtgttggc cgcgggtgac ttttggggcg gcgccggttc 1680

ggtggcttgc caggagttca ttacccagtt gggccgtaac ttccaggtga tctacgagca 1740
gg 1742

<210> 34
<211> 94
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.9A (MTI-A)

<400> 34
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1 5 10 15

Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
20 25 30

Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
35 40 45

Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50 55 60

Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80

Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85 90

<210> 35
<211> 585
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.8 (MSL)

<400> 35
tggattccga tagcggtttc ggcccctcga cgggcgacca cggcgcgcag gcctccgaac 60
gggggccgg gacgctggga ttcgccggga ccgcaaccaa agaacgccgg gtccgggcgg 120
tcgggctgac cgcactggcc ggtgatgagt tcggcaacgg cccccggatg ccgatggtgc 180
cggggacctg ggagcagggc agcaacgagc ccgaggcgcc cgacggatcg gggagagggg 240
gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggacccgtac 300
gggtcgaaag gagagatgtt atgagccttt tggatgctca tatcccacag ttggtggcct 360
cccagtcggc gtttgccgcc aaggcggggc tgatgcggca cacgatcggt caggccgagc 420
aggcggcgat gtcggctcag gcgtttcacc agggggagtc gtcggcggcg tttcaggccg 480
cccatgcccg gtttgtggcg gcggccgcca aagtcaacac cttgttggat gtcgcgcagg 540
cgaatctggg tgaggccgcc ggtacctatg tggccgccga tgctg 585

<210> 36
<211> 97
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.8 (MSL)

<400> 36
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
1 5 10 15

Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
20 25 30

Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
35 40 45

Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
50 55 60

Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
65 70 75 80

Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
85 90 95

Phe

<210> 37
<211> 500
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb8.4 (DPV)

<400> 37
cgtggcaatg tcgttgaccg tcggggccgg ggtcgcctcc gcagatcccg tggacgcggt 60
cattaacacc acctgcaatt acgggcaggt agtagctgcg ctcaacgcga cggatccggg 120
ggctgccgca cagttcaacg cctcaccggt ggcgcagtcc tatttgcgca atttcctcgc 180
cgcaccgcca cctcagcgcg ctgccatggc cgcgcaattg caagctgtgc cgggggcggc 240
acagtacatc ggccttgtcg agtcggttgc cggctcctgc aacaactatt aagcccatgc 300
gggccccatc ccgcgacccg gcatcgtcgc cggggctagg ccagattgcc ccgctcctca 360
acgggccgca tcccgcgacc cggcatcgtc gccggggcta ggccagattg ccccgctcct 420
caacgggccg catctcgtgc cgaattcctg cagcccgggg gatccactag ttctagagcg 480
gccgccaccg cggtggagct 500

<210> 38
<211> 96
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb8.4 (DPV)

<400> 38
Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1 5 10 15

Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
20 25 30

Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
35 40 45

Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
50 55 60

Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65 70 75 80

Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
85 90 95

<210> 39
<211> 999
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> DPEP

<400> 39
atgcatcacc atcaccatca catgcatcag gtggacccca acttgacacg tcgcaaggga 60
cgattggcgg cactggctat cgcggcgatg gccagcgcca gcctggtgac cgttgcggtg 120
cccgcgaccg ccaacgccga tccggagcca gcgcccccgg tacccacaac ggccgcctcg 180
ccgccgtcga ccgctgcagc gccacccgca ccggcgacac ctgttgcccc cccaccaccg 240
gacccgaacg caccgccgcc acctgtcatt gccccaaacg caccccaacc tgtccggatc 360
gacaacccgg ttggaggatt cagcttcgcg ctgcctgctg gctgggtgga gtctgacgcc 420
gcccacttcg actacggttc agcactcctc agcaaaacca ccggggaccc gccatttccc 480
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ctttacgcca gcgccgaagc caccgactcc aaggccgcgg cccggttggg ctcggacatg 600
ggtgagttct atatgcccta cccgggcacc cggatcaacc aggaaaccgt ctcgctcgac 660
gccaacgggg tgtctggaag cgcgtcgtat tacgaagtca agttcagcga tccgagtaag 720
ccgaacggcc agatctggac gggcgtaatc ggctcgcccg cggcgaacgc accggacgcc 780
gggccccctc agcgctggtt tgtggtatgg ctcgggaccg ccaacaaccc ggtggacaag 840
ggcgcggcca aggcgctggc cgaatcgatc cggcctttgg tcgccccgcc gccggcgccg 900
gcaccggctc ctgcagagcc cgctccggcg ccggcgccgg ccggggaagt cgctcctacc 960
ccgacgacac cgacaccgca gcggacctta ccggcctga 999

<210> 40
<211> 332
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> DPEP

<400> 40
Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1 5 10 15

Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20 25 30

Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35 40 45

Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50 55 60

Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65 70 75 80

Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85 90 95

Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100 105 110

Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
115 120 125

Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
130 135 140

Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145 150 155 160

Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
165 170 175

Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
180 185 190

Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
195 200 205

Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
210 215 220

Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
225 230 235 240

Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
245 250 255

Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
260 265 270

Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
275 280 285

Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
290 295 300

Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
305 310 315 320

Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
325 330

<210> 41
<400> 41
000

<210> 42
<400> 42
000

<210> 43
<211> 339
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> DPPD

<400> 43
atgaagttga agtttgctcg cctgagtact gcgatactgg gttgtgcagc ggcgcttgtg 60
tttcctgcct cggttgccag cgcagatcca cctgacccgc atcagccgga catgacgaaa 120
ggctattgcc cgggtggccg atggggtttt ggcgacttgg ccgtgtgcga cggcgagaag 180
taccccgacg gctcgttttg gcaccagtgg atgcaaacgt ggtttaccgg cccacagttt 240
tacttcgatt gtgtcagcgg cggtgagccc ctcccccggcc cgccgccacc gggtggttgc 300
ggtggggcaa ttccgtccga gcagcccaac gctccctga 339

<210> 44
<211> 112
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> DPPD

<400> 44
Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
1 5 10 15

Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
20 25 30

Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
35 40 45

Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
50 55 60

Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
65 70 75 80

Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
85 90 95

Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
100 105 110

<210> 45
<211> 154
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 45
atgacagagc agcagtggaa tttcgcgggt atcgaggccg cggcaagcgc aatccaggga 60
aatgtcacgt ccattcattc cctccttgac gaggggaagc agtccctgac caagctcgca 120
gcggcctggg gcggtagcgg ttcggaagcg tacc 154

<210> 46
<211> 51
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> ESAT-6

<400> 46
Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1 5 10 15

Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
20 25 30

Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
35 40 45

Glu Ala Tyr
50

<210> 47
<211> 2310
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb82

<400> 47
ccagcccccg ccccgcccac gccgaggtat gtggactgat ggccaaagcg tcagagaccg 60
aacgttcggg ccccggcacc caaccggcgg acgcccagac cgcgacgtcc gcgacggttc 120
gacccctgag cacccaggcg gtgttccgcc ccgatttcgg cgatgaggac aacttccccc 180
atccgacgct cggcccggac accgagccgc aagaccggat ggccaccacc agccgggtgc 240
gcccgccggt cagacggctg ggcggcggcc tggtggaaat cccgcgggcg cccgatatcg 300
atccgcttga ggccctgatg accaacccgg tggtgccgga gtccaagcgg ttctgctgga 360
actgtggacg tcccgtcggc cggtccgact cggagaccaa gggagcttca gagggctggt 420
gtccctattg cggcagcccg tattcgttcc tgccgcagct aaatcccggg gacatcgtcg 480
ccggccagta cgaggtcaaa ggctgcatcg cgcacggcgg actgggctgg atctacctcg 540
ctctcgaccg caatgtcaac ggccgtccgg tggtgctcaa gggcctggtg cattccggtg 600
atgccgaagc gcaggcaatg gcgatggccg aacgccagtt cctggccgag gtggtgcacc 660
cgtcgatcgt gcagatcttc aactttgtcg agcacaccga caggcacggg gatccggtcg 720
gctacatcgt gatggaatac gtcggcgggc aatcgctcaa acgcagcaag ggtcagaaac 780
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tctacaccgt gggacgcacg ctcgcggcgc tcacgctgga cctgcccacc cgcaatggcc 1080
gttatgtgga tgggctaccc gaagacgacc cggtgctgaa aacctacgac tcttacggcc 1140
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aacacaagtt ctatcagacg gtgtggagca ccaacgacgg cgtgatctcg gcggctttcg 1860
gactggccag agcccggtcg gccgaaggtg atcgggtcgg cgccgtgcgc acgctcgacg 1920
aggtaccgcc cacttctcgg catttcacca cggcacggct gaccagcgcg gtgactctgt 1980
tgtccggccg gtcaacgagt gaagtcaccg aggaacagat ccgcgacgcc gcccgaagag 2040
tggaggcgct gccccgacc gaaccacgcg tgctgcagat ccgcgccctg gtgctgggtg 2100
gcgcgctgga ctggctgaag gacaacaagg ccagcaccaa ccacatcctc ggtttcccgt 2160
tcaccagtca cgggctgcgg ctgggtgtcg aggcgtcact gcgcagcctg gcccgggtag 2220
ctcccactca acggcatcgc tacacgctgg tggacatggc caacaaggtc cggcccacca 2280
gcacgttcta agccgcccga gtgtgaatcg 2310

<210> 48
<211> 750
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb82

<400> 48
Met Ala Lys Ala Ser Glu Thr Glu Arg Ser Gly Pro Gly Thr Gln Pro
1 5 10 15

Ala Asp Ala Gln Thr Ala Thr Ser Ala Thr Val Arg Pro Leu Ser Thr
20 25 30

Gln Ala Val Phe Arg Pro Asp Phe Gly Asp Glu Asp Asn Phe Pro His
35 40 45

Pro Thr Leu Gly Pro Asp Thr Glu Pro Gln Asp Arg Met Ala Thr Thr
50 55 60

Ser Arg Val Arg Pro Pro Val Arg Arg Leu Gly Gly Gly Leu Val Glu
65 70 75 80

Ile Pro Arg Ala Pro Asp Ile Asp Pro Leu Glu Ala Leu Met Thr Asn
85 90 95

Pro Val Val Pro Glu Ser Lys Arg Phe Cys Trp Asn Cys Gly Arg Pro
100 105 110

Val Gly Arg Ser Asp Ser Glu Thr Lys Gly Ala Ser Glu Gly Trp Cys
115 120 125

Pro Tyr Cys Gly Ser Pro Tyr Ser Phe Leu Pro Gln Leu Asn Pro Gly
130 135 140

Asp Ile Val Ala Gly Gln Tyr Glu Val Lys Gly Cys Ile Ala His Gly
145 150 155 160

Gly Leu Gly Trp Ile Tyr Leu Ala Leu Asp Arg Asn Val Asn Gly Arg
165 170 175

Pro Val Val Leu Lys Gly Leu Val His Ser Gly Asp Ala Glu Ala Gln
180 185 190

Ala Met Ala Met Ala Glu Arg Gln Phe Leu Ala Glu Val Val His Pro
195 200 205

Ser Ile Val Gln Ile Phe Asn Phe Val Glu His Thr Asp Arg His Gly
210 215 220

Asp Pro Val Gly Tyr Ile Val Met Glu Tyr Val Gly Gly Gln Ser Leu
225 230 235 240

Lys Arg Ser Lys Gly Gln Lys Leu Pro Val Ala Glu Ala Ile Ala Tyr
245 250 255

Leu Leu Glu Ile Leu Pro Ala Leu Ser Tyr Leu His Ser Ile Gly Leu
260 265 270

Val Tyr Asn Asp Leu Lys Pro Glu Asn Ile Met Leu Thr Glu Glu Gln
275 280 285

Leu Lys Leu Ile Asp Leu Gly Ala Val Ser Arg Ile Asn Ser Phe Gly
290 295 300

Tyr Leu Tyr Gly Thr Pro Gly Phe Gln Ala Pro Glu Ile Val Arg Thr
305 310 315 320

Gly Pro Thr Val Ala Thr Asp Ile Tyr Thr Val Gly Arg Thr Leu Ala
325 330 335

Ala Leu Thr Leu Asp Leu Pro Thr Arg Asn Gly Arg Tyr Val Asp Gly
340 345 350

Leu Pro Glu Asp Asp Pro Val Leu Lys Thr Tyr Asp Ser Tyr Gly Arg
355 360 365

Leu Leu Arg Arg Ala Ile Asp Pro Asp Pro Arg Gln Arg Phe Thr Thr
370 375 380

Ala Glu Glu Met Ser Ala Gln Leu Thr Gly Val Leu Arg Glu Val Val
385 390 395 400

Ala Gln Asp Thr Gly Val Pro Arg Pro Gly Leu Ser Thr Ile Phe Ser
405 410 415

Pro Ser Arg Ser Thr Phe Gly Val Asp Leu Leu Val Ala His Thr Asp
420 425 430

Val Tyr Leu Asp Gly Gln Val His Ala Glu Lys Leu Thr Ala Asn Glu
435 440 445

Ile Val Thr Ala Leu Ser Val Pro Leu Val Asp Pro Thr Asp Val Ala
450 455 460

Ala Ser Val Leu Gln Ala Thr Val Leu Ser Gln Pro Val Gln Thr Leu
465 470 475 480

Asp Ser Leu Arg Ala Ala Arg His Gly Ala Leu Asp Ala Asp Gly Val
485 490 495

Asp Phe Ser Glu Ser Val Glu Leu Pro Leu Met Glu Val Arg Ala Leu
500 505 510

Leu Asp Leu Gly Asp Val Ala Lys Ala Thr Arg Lys Leu Asp Asp Leu
515 520 525

Ala Glu Arg Val Gly Trp Arg Trp Arg Leu Val Trp Tyr Arg Ala Val
530 535 540

Ala Glu Leu Leu Thr Gly Asp Tyr Asp Ser Ala Thr Lys His Phe Thr
545 550 555 560

Glu Val Leu Asp Thr Phe Pro Gly Glu Leu Ala Pro Lys Leu Ala Leu
565 570 575

Ala Ala Thr Ala Glu Leu Ala Gly Asn Thr Asp Glu His Lys Phe Tyr
580 585 590

Gln Thr Val Trp Ser Thr Asn Asp Gly Val Ile Ser Ala Ala Phe Gly
595 600 605

Leu Ala Arg Ala Arg Ser Ala Glu Gly Asp Arg Val Gly Ala Val Arg
610 615 620

Thr Leu Asp Glu Val Pro Pro Thr Ser Arg His Phe Thr Thr Ala Arg
625 630 635 640

Leu Thr Ser Ala Val Thr Leu Leu Ser Gly Arg Ser Thr Ser Glu Val
645 650 655

Thr Glu Glu Gln Ile Arg Asp Ala Ala Arg Arg Val Glu Ala Leu Pro
660 665 670

Pro Thr Glu Pro Arg Val Leu Gln Ile Arg Ala Leu Val Leu Gly Gly
675 680 685

Ala Leu Asp Trp Leu Lys Asp Asn Lys Ala Ser Thr Asn His Ile Leu
690 695 700

Gly Phe Pro Phe Thr Ser His Gly Leu Arg Leu Gly Val Glu Ala Ser
705 710 715 720

Leu Arg Ser Leu Ala Arg Val Ala Pro Thr Gln Arg His Arg Tyr Thr
725 730 735

Leu Val Asp Met Ala Asn Lys Val Arg Pro Thr Ser Thr Phe
740 745 750

<210> 49
<211> 1920
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb59

<400> 49
cacgactgcc cgactgaacc cgaactagtc agcacaaacc gaagtaggaa gacgaaaagc 60
tatggctgag ttgacaatcc ccgctgatga catccagagc gcaatcgaag agtacgtaag 120
ctctttcacc gccgacacca gtagagagga agtcggtacc gtcgtcgatg ccggggacgg 180
catcgcacac gtcgagggtt tgccatcggt gatgacccaa gagctgctcg aattcccggg 240
cggaatcctc ggcgtcgccc tcaacctcga cgagcacagc gtcggcgcgg tgatcctcgg 300
tgacttcgag aacatcgaag aaggtcagca ggtcaagcgc accggcgaag tcttatcggt 360
tccggttggc gacgggtttt tggggcgggt ggttaacccg ctcggccagc cgatcgacgg 420
gcgcggagac gtcgactccg atactcggcg cgcgctggag ctccaggcgc cctcggtggt 480
gcaccggcaa ggcgtgaagg agccgttgca gaccgggatc aaggcgattg acgcgatgac 540
cccgatcggc cgcggccagc gccagctgat catcggcgac cgcaagaccg gcaaaaccgc 600
cgtctgcgtc gacaccatcc tcaaccagcg gcagaactgg gagtccggtg atcccaagaa 660
gcaggtgcgc tgtgtatacg tggccatcgg gcagaaggga actaccatcg ccgcggtacg 720

ccgcacactg gaagagggcg gtgcgatgga ctacaccacc atcgtcgcgg ccgcggcgtc 780
ggagtccgcc ggtttcaaat ggcttgcgcc gtacaccggt tcggcgatcg cccagcactg 840
gatgtacgag ggcaagcatg tgctgatcat cttcgacgac ctgactaagc aggccgaggc 900
ataccgggcg atctcgctgc tgctgcgccg tccgcccggc cgtgaggcct accccggcga 960
tgtgttctat ctgcattcgc ggcttttgga gcgctgcgcc aaactgtccg acgatctcgg 1020
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catcccgacc aacgtcatct cgatcaccga cgggcaatgt ttcctggaaa ccgacctgtt 1140
caaccagggc gtccggccgg ccatcaacgt cggtgtgtcg gtgtcccgag tcggcggcgc 1200
ggcgcagatc aaggctatga aagaggtcgc cggaagcctc cgcttggacc tttcgcaata 1260
ccgcgagcta gaagctttcg ccgctttcgc ttctgatttg gacgccgcat cgaaggcgca 1320
gttggagcgc ggcgcccggc tggtcgagct gctcaagcag ccgcaatccc agcccatgcc 1380
cgttgaggag caagtggttt cgatcttcct gggcaccggc ggtcacctgg actcggtgcc 1440
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agagattttg actgagatcc gggacagcca aaagctcacc gaggaggccg ccgacaagct 1560
caccgaggtc atcaagaact tcaagaaggg cttcgcggcc accggtggcg gctctgtggt 1620
gcccgacgaa catgtcgagg ccctcgacga ggataagctc gccaaggaag ccgtgaaggt 1680
caaaaagccg gcgccgaaga agaagaaata gctaaccatg gctgccacac ttcgcgaact 1740
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tgcgacatcg cgcatcgcca gggcgcaggc tcggctcgag tccgctcggc cctacgcttt 1860
tgagatcacc cggatgctta ccaccctggc cgctgaagcc gcactggacc atccgttgct 1920

<210> 50
<211> 549
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> Mtb59

<400> 50
Met Ala Glu Leu Thr Ile Pro Ala Asp Asp Ile Gln Ser Ala Ile Glu
1 5 10 15

Glu Tyr Val Ser Ser Phe Thr Ala Asp Thr Ser Arg Glu Glu Val Gly
20 25 30

Thr Val Val Asp Ala Gly Asp Gly Ile Ala His Val Glu Gly Leu Pro
35 40 45

Ser Val Met Thr Gln Glu Leu Leu Glu Phe Pro Gly Gly Ile Leu Gly
50 55 60

Val Ala Leu Asn Leu Asp Glu His Ser Val Gly Ala Val Ile Leu Gly
65 70 75 80

Asp Phe Glu Asn Ile Glu Glu Gly Gln Gln Val Lys Arg Thr Gly Glu
85 90 95

Val Leu Ser Val Pro Val Gly Asp Gly Phe Leu Gly Arg Val Val Asn
100 105 110

Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr
115 120 125

Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val His Arg Gln Gly
130 135 140

Val Lys Glu Pro Leu Gln Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
145 150 155 160

Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
165 170 175

Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Arg Gln Asn
180 185 190

Trp Glu Ser Gly Asp Pro Lys Lys Gln Val Arg Cys Val Tyr Val Ala
195 200 205

Ile Gly Gln Lys Gly Thr Thr Ile Ala Ala Val Arg Arg Thr Leu Glu
210 215 220

Glu Gly Gly Ala Met Asp Tyr Thr Thr Ile Val Ala Ala Ala Ala Ser
225 230 235 240

Glu Ser Ala Gly Phe Lys Trp Leu Ala Pro Tyr Thr Gly Ser Ala Ile
245 250 255

Ala Gln His Trp Met Tyr Glu Gly Lys His Val Leu Ile Ile Phe Asp
260 265 270

Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu
275 280 285

Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu
290 295 300

His Ser Arg Leu Leu Glu Arg Cys Ala Lys Leu Ser Asp Asp Leu Gly
305 310 315 320

Gly Gly Ser Leu Thr Gly Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp
325 330 335

Ile Ser Ala Tyr Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
340 345 350

Cys Phe Leu Glu Thr Asp Leu Phe Asn Gln Gly Val Arg Pro Ala Ile
355 360 365

Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Ile Lys
370 375 380

Ala Met Lys Glu Val Ala Gly Ser Leu Arg Leu Asp Leu Ser Gln Tyr
385 390 395 400

Arg Glu Leu Glu Ala Phe Ala Ala Phe Ala Ser Asp Leu Asp Ala Ala
405 410 415

Ser Lys Ala Gln Leu Glu Arg Gly Ala Arg Leu Val Glu Leu Leu Lys
420 425 430

Gln Pro Gln Ser Gln Pro Met Pro Val Glu Glu Gln Val Val Ser Ile
435 440 445

Phe Leu Gly Thr Gly Gly His Leu Asp Ser Val Pro Val Glu Asp Val
450 455 460

Arg Arg Phe Glu Thr Glu Leu Leu Asp His Met Arg Ala Ser Glu Glu
465 470 475 480

Glu Ile Leu Thr Glu Ile Arg Asp Ser Gln Lys Leu Thr Glu Glu Ala
485 490 495

Ala Asp Lys Leu Thr Glu Val Ile Lys Asn Phe Lys Lys Gly Phe Ala
500 505 510

Ala Thr Gly Gly Gly Ser Val Val Pro Asp Glu His Val Glu Ala Leu
515 520 525

Asp Glu Asp Lys Leu Ala Lys Glu Ala Val Lys Val Lys Lys Pro Ala
530 535 540

Pro Lys Lys Lys Lys
545

<210> 51
<211> 3523
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TbF14 fusion protein

<400> 51
atgcagcatc accaccatca ccacactgat cgcgtgtcgg tgggcaactt gcgcatcgct 60
cgggtgctct acgacttcgt gaacaatgaa gccctgcctg gcaccgatat cgacccggac 120
agcttctggg cgggcgtcga caaggtcgtc gccgacctga ccccgcagaa ccaagctctg 180
ttgaacgccc gcgacgagct gcaggcgcag atcgacaagt ggcaccggcg tcgggtgatc 240
gagcccatcg acatggatgc ctaccgccag ttcctcaccg agatcggcta cctgcttccc 300
gaacctgatg acttcaccat caccacgtcc ggtgtcgacg ctgagatcac cacgaccgcc 360
ggcccccagc tggtggtgcc ggtgctcaac gcgcggtttg ctctgaacgc ggccaacgct 420
cgctggggct ccctctacga cgccttgtat ggcaccgatg tcatccccga gaccgacggc 480
gccgaaaaag gccccacgta caacaaggtt cgtggcgaca aggtgatcgc gtatgcccgc 540
aagttcctcg acgacagtgt tccgctgtcg tcgggttcct ttggcgacgc caccggtttc 600
acagtgcagg atggccagct cgtggttgcc ttgccggata agtccaccgg cctggccaac 660
cccggccagt tcgccggcta caccggcgca gccgagtcgc cgacatcggt gctgctaatc 720
aatcacggtt tgcacatcga gatcctgatc gatccggagt cgcaggtcgg caccaccgac 780
cgggccggcg tcaaggacgt gatcctggaa tccgcgatca ccacgatcat ggacttcgag 840
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ctgaacaagg gcgacctggc agcagcggta gacaaggacg gcaccgcttt cctgcgggtg 960
ctcaataggg accggaacta caccgcaccc ggcggtggcc agttcacgct gcctggacgc 1020
agcctcatgt tcgtccgcaa cgtcggtcac ttgatgacga atgacgccat cgtcgacact 1080
gacggcagcg aggtgttcga aggcatcatg gatgccctat tcaccggcct gatcgccatc 1140
cacgggctaa aggccagcga cgtcaacggg ccgctgatca acagccgcac cggctccatc 1200
tacatcgtca agccgaagat gcacggtccg gccgaggtgg cgtttacctg cgaactgttc 1260
agccgggttg aagatgtgct ggggttgccg caaaacacca tgaagatcgg catcatggac 1320
gaggaacgcc ggaccacggt caacctcaag gcgtgcatca aagctgccgc ggaccgcgtg 1380
gtgttcatca acaccgggtt cctggaccgc accggcgatg aaatccacac ctcgatggag 1440
gccggcccga tggtgcgcaa gggcaccatg aagagccagc cgtggatctt ggcctacgag 1500
gaccacaacg tcgatgccgg cctggccgcc gggttcagcg gccgagccca ggtcggcaag 1560
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cgcgccgggg ccagcaccgc ctgggttccc tctcccactg cggccaccct gcatgcgctg 1680
cactaccacc aggtcgacgt cgccgcggtg caacaaggac tggcggggaa gcgtcgcgcc 1740
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cgggccacgc tgcgaatctc cagccaattg ttggccaact ggctgcgcca cggtgtgatc 1980
accagcgcgg atgtgcgggc cagcttggag cggatggcgc cgttggtcga tcgacaaaac 2040
gcgggcgacg tggcataccg accgatggca cccaacttcg acgacagtat cgccttcctg 2100

gccgcgcagg agctgatctt gtccggggcc cagcagccca acggctacac cgagccgatc 2160
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agggccggtg acgatgcggc cagggtgcag aagtacggcg gatcctcggt ggccgacgcc 2280
gaacggattc gccgcgtcgc cgaacgcatc gtcgccacca agaagcaagg caatgacgtc 2340
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gctgcagaac gtctccaagg tcgaggacgg caagaccgac atcaccttca cctgctcccg 3180
cagacgtcgg gcccgccgcc gtggaaaaac tggactcgct cagaaacgag atcggcttct 3240
acacagctgc tgtacgacga ccacatcggc aaggtatcgc tgatcggtgc cggcatgcgc 3300
agccaccccg gggtcaccgc gacgttctgt gaggcgctgg cggcggtggg ggtcaacatc 3360
gagctgatct ccacctcgga agatcagaga tctcggtgtt gtgccgcgac accgaactgg 3420
acaaggccgt ggtcgcgctg catgaagcgt tcgggctcgg cggcgacgag gaggccacgg 3480
tgtacgcggg gacgggacgg tagatgggcc tgtcaatagt gaa 3523

<210> 52
<211> 1172
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TbF14 fusion protein

<400> 52
Met Gln His His His His His His Thr Asp Arg Val Ser Val Gly Asn
1 5 10 15

Leu Arg Ile Ala Arg Val Leu Tyr Asp Phe Val Asn Asn Glu Ala Leu
20 25 30

Pro Gly Thr Asp Ile Asp Pro Asp Ser Phe Trp Ala Gly Val Asp Lys
35 40 45

Val Val Ala Asp Leu Thr Pro Gln Asn Gln Ala Leu Leu Asn Ala Arg
50 55 60

Asp Glu Leu Gln Ala Gln Ile Asp Lys Trp His Arg Arg Arg Val Ile
65 70 75 80

Glu Pro Ile Asp Met Asp Ala Tyr Arg Gln Phe Leu Thr Glu Ile Gly
85 90 95

Tyr Leu Leu Pro Glu Pro Asp Asp Phe Thr Ile Thr Thr Ser Gly Val
100 105 110

Asp Ala Glu Ile Thr Thr Thr Ala Gly Pro Gln Leu Val Val Pro Val
115 120 125

Leu Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser
130 135 140

Leu Tyr Asp Ala Leu Tyr Gly Thr Asp Val Ile Pro Glu Thr Asp Gly
145 150 155 160

Ala Glu Lys Gly Pro Thr Tyr Asn Lys Val Arg Gly Asp Lys Val Ile
165 170 175

Ala Tyr Ala Arg Lys Phe Leu Asp Asp Ser Val Pro Leu Ser Ser Gly
180 185 190

Ser Phe Gly Asp Ala Thr Gly Phe Thr Val Gln Asp Gly Gln Leu Val
195 200 205

Val Ala Leu Pro Asp Lys Ser Thr Gly Leu Ala Asn Pro Gly Gln Phe
210 215 220

Ala Gly Tyr Thr Gly Ala Ala Glu Ser Pro Thr Ser Val Leu Leu Ile
225 230 235 240

Asn His Gly Leu His Ile Glu Ile Leu Ile Asp Pro Glu Ser Gln Val
245 250 255

Gly Thr Thr Asp Arg Ala Gly Val Lys Asp Val Ile Leu Glu Ser Ala
260 265 270

Ile Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala
275 280 285

Ala Asp Lys Val Leu Gly Tyr Arg Asn Trp Leu Gly Leu Asn Lys Gly
290 295 300

Asp Leu Ala Ala Ala Val Asp Lys Asp Gly Thr Ala Phe Leu Arg Val
305 310 315 320

Leu Asn Arg Asp Arg Asn Tyr Thr Ala Pro Gly Gly Gly Gln Phe Thr
325 330 335

Leu Pro Gly Arg Ser Leu Met Phe Val Arg Asn Val Gly His Leu Met
340 345 350

Thr Asn Asp Ala Ile Val Asp Thr Asp Gly Ser Glu Val Phe Glu Gly
355 360 365

Ile Met Asp Ala Leu Phe Thr Gly Leu Ile Ala Ile His Gly Leu Lys
370 375 380

Ala Ser Asp Val Asn Gly Pro Leu Ile Asn Ser Arg Thr Gly Ser Ile
385 390 395 400

Tyr Ile Val Lys Pro Lys Met His Gly Pro Ala Glu Val Ala Phe Thr
405 410 415

Cys Glu Leu Phe Ser Arg Val Glu Asp Val Leu Gly Leu Pro Gln Asn
420 425 430

Thr Met Lys Ile Gly Ile Met Asp Glu Glu Arg Arg Thr Thr Val Asn
435 440 445

Leu Lys Ala Cys Ile Lys Ala Ala Ala Asp Arg Val Val Phe Ile Asn
450 455 460

Thr Gly Phe Leu Asp Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu
465 470 475 480

Ala Gly Pro Met Val Arg Lys Gly Thr Met Lys Ser Gln Pro Trp Ile
485 490 495

Leu Ala Tyr Glu Asp His Asn Val Asp Ala Gly Leu Ala Ala Gly Phe
500 505 510

Ser Gly Arg Ala Gln Val Gly Lys Gly Met Trp Thr Met Thr Glu Leu
515 520 525

Met Ala Asp Met Val Glu Thr Lys Ile Ala Gln Pro Arg Ala Gly Ala
530 535 540

Ser Thr Ala Trp Val Pro Ser Pro Thr Ala Ala Thr Leu His Ala Leu
545 550 555 560

His Tyr His Gln Val Asp Val Ala Ala Val Gln Gln Gly Leu Ala Gly
565 570 575

Lys Arg Arg Ala Thr Ile Glu Gln Leu Leu Thr Ile Pro Leu Ala Lys
580 585 590

Glu Leu Ala Trp Ala Pro Asp Glu Ile Arg Glu Glu Val Asp Asn Asn
595 600 605

Cys Gln Ser Ile Leu Gly Tyr Val Val Arg Trp Val Asp Gln Gly Val
610 615 620

Gly Cys Ser Lys Val Pro Asp Ile His Asp Val Ala Leu Met Glu Asp
625 630 635 640

Arg Ala Thr Leu Arg Ile Ser Ser Gln Leu Leu Ala Asn Trp Leu Arg
645 650 655

His Gly Val Ile Thr Ser Ala Asp Val Arg Ala Ser Leu Glu Arg Met
660 665 670

Ala Pro Leu Val Asp Arg Gln Asn Ala Gly Asp Val Ala Tyr Arg Pro
675 680 685

Met Ala Pro Asn Phe Asp Asp Ser Ile Ala Phe Leu Ala Ala Gln Glu
690 695 700

Leu Ile Leu Ser Gly Ala Gln Gln Pro Asn Gly Tyr Thr Glu Pro Ile
705 710 715 720

Leu His Arg Arg Arg Arg Glu Phe Lys Ala Arg Ala Ala Glu Lys Pro
725 730 735

Ala Pro Ser Asp Arg Ala Gly Asp Asp Ala Ala Arg Val Gln Lys Tyr
740 745 750

Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg Val Ala Glu
755 760 765

Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val Val Val Val
770 775 780

Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu Ala Gln Gln
785 790 795 800

Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu Leu Thr Ala
805 810 815

Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile Glu Ser Leu
820 825 830

Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly Val Ile Thr
835 840 845

Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr Pro Gly Arg
850 855 860

Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu Val Ala Gly Phe
865 870 875 880

Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu Gly Arg Gly
885 890 895

Gly Ser Asp Thr Thr Ala Val Ala Met Ala Ala Ala Leu Gly Ala Asp
900 905 910

Val Cys Glu Ile Tyr Thr Asp Val Asp Gly Ile Phe Ser Ala Asp Pro
915 920 925

Arg Ile Val Arg Asn Ala Arg Lys Leu Asp Thr Val Thr Phe Glu Glu
930 935 940

Met Leu Glu Met Ala Ala Cys Gly Ala Lys Val Leu Met Leu Arg Cys
945 950 955 960

Val Glu Tyr Ala Arg Arg His Asn Ile Pro Val His Val Arg Ser Ser
965 970 975

Tyr Ser Asp Arg Pro Gly Thr Val Val Val Gly Ser Ile Lys Asp Val
980 985 990

Pro Met Glu Asp Pro Ile Leu Thr Gly Val Ala His Asp Arg Ser Glu
995 1000 1005

Ala Lys Val Thr Ile Val Gly Leu Pro Asp Ile Pro Gly Tyr Ala Ala
1010 1015 1020

Lys Val Phe Arg Ala Val Ala Arg Arg Arg Arg Gln His Arg His Gly
1025 1030 1035 1040

Ala Ala Glu Arg Leu Gln Gly Arg Gly Arg Gln Asp Arg His His Leu
1045 1050 1055

His Leu Leu Pro Gln Thr Ser Gly Pro Pro Pro Trp Lys Asn Trp Thr
1060 1065 1070

Arg Ser Glu Thr Arg Ser Ala Ser Thr Gln Leu Leu Tyr Asp Asp His
1075 1080 1085

Ile Gly Lys Val Ser Leu Ile Gly Ala Gly Met Arg Ser His Pro Gly
1090 1095 1100

Val Thr Ala Thr Phe Cys Glu Ala Leu Ala Ala Val Gly Val Asn Ile
1105 1110 1115 1120

Glu Leu Ile Ser Thr Ser Glu Asp Gln Arg Ser Arg Cys Cys Ala Ala
1125 1130 1135

Thr Pro Asn Trp Thr Arg Pro Trp Ser Arg Cys Met Lys Arg Ser Gly
1140 1145 1150

Ser Ala Ala Thr Arg Arg Pro Arg Cys Thr Arg Gly Arg Asp Gly Arg
1155 1160 1165

Trp Ala Cys Gln
1170

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<211> 2952
<212> DNA
<213> Artificial Sequence

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gaacaggcgg cggcggaggc ggtccagcgg gcgcgggata gcgtcgatga catccgcgtc 120
gctcgggtca ttgagcagga catggccgtg gacagcgccg gcaagatcac ctaccgcatc 180
aagctcgaag tgtcgttcaa gatgaggccg gcgcaaccga ggtgtggctc gaaaccaccg 240
agcggttcgc ctgaaacggg cgccggcgcc ggtactgtcg cgactacccc cgcgtcgtcg 300
ccggtgacgt tggcggagac cggtagcacg ctgctctacc cgctgttcaa cctgtggggt 360
ccggcctttc acgagaggta tccgaacgtc acgatcaccg ctcagggcac cggttctggt 420
gccgggatcg cgcaggccgc cgccgggacg gtcaacattg gggcctccga cgcctatctg 480
tcggaaggtg atatggccgc gcacaagggg ctgatgaaca tcgcgctagc catctccgct 540
cagcaggtca actacaacct gcccggagtg agcgagcacc tcaagctgaa cggaaaagtc 600
ctggcggcca tgtaccaggg caccatcaaa acctgggacg acccgcagat cgctgcgctc 660
aaccccggcg tgaacctgcc cggcaccgcg gtagttccgc tgcaccgctc cgacgggtcc 720
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tcgcccggct tcggcaccac cgtcgacttc ccggcggtgc cgggtgcgct gggtgagaac 840
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tcgaaaaccc cggcgaacca ggcgatttcg atgatcgacg ggcccgcccc ggacggctac 1080
ccgatcatca actacgagta cgccatcgtc aacaaccggc aaaaggacgc cgccaccgcg 1140
cagaccttgc aggcatttct gcactgggcg atcaccgacg gcaacaaggc ctcgttcctc 1200
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cgtcaggccg gcgtccaata ctcgagggcc gacgaggagc agcagcaggc gctgtcctcg 1560
caaatgggct ttactcagtc gcagaccgtg acggtggatc agcaagagat tttgaacagg 1620
gccaacgagg tggaggcccc gatggcggac ccaccgactg atgtccccat cacaccgtgc 1680
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gatacgccga gggtggccac ggccggtgaa cccaacttca tggatctcaa agaagcggca 1980
aggaagctcg aaacgggcga ccaaggcgca tcgctcgcgc actttgcgga tgggtggaac 2040
actttcaacc tgacgctgca aggcgacgtc aagcggttcc gggggtttga caactgggaa 2100
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tgggctaggc gggaacatcc gacttatgaa gacatagtcg ggctcgaacg gctttacgcg 2280
gaaaaccctt cggcccgcga ccaaattctc ccggtgtacg cggagtatca gcagaggtcg 2340
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gcaccgatgg ttccgcctac cggatcgccg ggtggtggcc tcccggctga cacggcggcg 2580
cagctgacgt cggctgggcg ggaagccgca gcgctgtcgg gcgacgtggc ggtcaaagcg 2640
gcatcgctcg gtggcggtgg aggcggcggg gtgccgtcgg cgccgttggg atccgcgatc 2700
gggggcgccg aatcggtgcg gcccgctggc gctggtgaca ttgccggctt aggccaggga 2760
agggccggcg gcggcgccgc gctgggcggc ggtggcatgg gaatgccgat gggtgccgcg 2820
catcagggac aagggggcgc caagtccaag ggttctcagc aggaagacga ggcgctctac 2880
accgaggatc gggcatggac cgaggccgtc attggtaacc gtcggcgcca ggacagtaag 2940
gagtcgaagt ga 2952

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<211> 983
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence:TbF15 fusion protein

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Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
20 25 30

Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
35 40 45

Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
50 55 60

Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Cys Gly Ser Lys Pro Pro
65 70 75 80

Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr
85 90 95

Pro Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu
100 105 110

Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro
115 120 125

Asn Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala
130 135 140

Gln Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu
145 150 155 160

Ser Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu
165 170 175

Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu
180 185 190

His Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr
195 200 205

Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val
210 215 220

Asn Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser
225 230 235 240

Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu
245 250 255

Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala
260 265 270

Val Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly
275 280 285

Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu
290 295 300

Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser
305 310 315 320

Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala
325 330 335

Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile
340 345 350

Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala
355 360 365

Ile Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln
370 375 380

Ala Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu
385 390 395 400

Asp Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser
405 410 415

Asp Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala
420 425 430

Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp
435 440 445

Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln
450 455 460

Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val
465 470 475 480

Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile
485 490 495

Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu
500 505 510

Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Thr Gln Ser Gln
515 520 525

Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn Arg Ala Asn Glu Val
530 535 540

Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val Pro Ile Thr Pro Cys
545 550 555 560

Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln Leu Val Leu Ser Ala
565 570 575

Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala Lys Glu Arg Gln Arg
580 585 590

Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala Tyr Gly Glu Val Asp
595 600 605

Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly Glu Gly Thr Val Gln
610 615 620

Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser Ser Ala Glu Leu Thr
625 630 635 640

Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro Asn Phe Met Asp Leu
645 650 655

Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp Gln Gly Ala Ser Leu
660 665 670

Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn Leu Thr Leu Gln Gly
675 680 685

Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp Glu Gly Asp Ala Ala
690 695 700

Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg Gln Trp Ile Leu His
705 710 715 720

Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln Ala Gln Tyr Val Ala
725 730 735

Gln Leu His Val Trp Ala Arg Arg Glu His Pro Thr Tyr Glu Asp Ile
740 745 750

Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro Ser Ala Arg Asp Gln
755 760 765

Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg Ser Glu Lys Val Leu
770 775 780

Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro Val Asn Pro Pro Lys
785 790 795 800

Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro Pro Pro Gln Glu Gln
805 810 815

Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser Asp Gly Ser Gly Val
820 825 830

Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met Val Pro Pro Thr Gly
835 840 845

Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala Ala Gln Leu Thr Ser
850 855 860

Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp Val Ala Val Lys Ala
865 870 875 880

Ala Ser Leu Gly Gly Gly Gly Gly Gly Gly Val Pro Ser Ala Pro Leu
885 890 895

Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg Pro Ala Gly Ala Gly
900 905 910

Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly Gly Gly Ala Ala Leu
915 920 925

Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala Ala His Gln Gly Gln
930 935 940

Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu Asp Glu Ala Leu Tyr
945 950 955 960

Thr Glu Asp Arg Ala Trp Thr Glu Ala Val Ile Gly Asn Arg Arg Arg
965 970 975

Gln Asp Ser Lys Glu Ser Lys
980

<210> 55
<400> 55
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<210> 56
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<210> 57
<211> 2232
<212> DNA
<213> Artificial Sequence

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HTCC#1(184-392)-TbH9-HTCC#1(1-129)

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<400> 57

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    Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly
      1               5                  10                  15

acc ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg   96
Thr Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu
                20                  25                  30

aaa gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct  144
Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser
            35                  40                  45

cga ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg  192
Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu
        50                  55                  60

acc ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg  240
Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala
    65                  70                  75

gcc ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg  288
Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala
80                  85                  90                  95

agc tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt  336
Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly
                100                 105                 110

ttt ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg  384
Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg
            115                 120                 125

cag gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag  432
Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu
        130                 135                 140

cag gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt  480
Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly
    145                 150                 155

atg ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg  528
Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala
160                 165                 170                 175

tcg aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc  576
Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly
                180                 185                 190

act gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg  624
Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly
            195                 200                 205

caa aag gtg ctg gta cga aac gtc gtc gaa ttc atg gtg gat ttc ggg  672
Gln Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly
        210                 215                 220

gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt  720
Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly
    225                 230                 235
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tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt   768
Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser
240                 245                 250                 255

gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg   816
Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu
                260                 265                 270

acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg   864
Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala
            275                 280                 285

gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag   912
Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu
        290                 295                 300

ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg   960
Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala
    305                 310                 315

tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa  1008
Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu
320                 325                 330                 335

ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg  1056
Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala
                340                 345                 350

atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc  1104
Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala
            355                 360                 365

gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg gcg acg gcg acg  1152
Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr
        370                 375                 380

ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc  1200
Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu
    385                 390                 395

ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg  1248
Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala
400                 405                 410                 415

aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag  1296
Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln
                420                 425                 430

ccc acg cag ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag  1344
Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys
            435                 440                 445

acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc  1392
Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala
        450                 455                 460

aac aac cac atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc  1440
Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr
    465                 470                 475
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ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag gcc   1488
Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala
480                 485                 490                 495

gtg caa acc gcg gcg caa aac ggg gtc cgg gcg atg agc tcg ctg ggc   1536
Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly
                500                 505                 510

agc tcg ctg ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg   1584
Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu
            515                 520                 525

ggt cgg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc   1632
Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala
        530                 535                 540

gcg gcc aac cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg ctg acc   1680
Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr
    545                 550                 555

agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg   1728
Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly
560                 565                 570                 575

ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt   1776
Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly
                580                 585                 590

gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca   1824
Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala
            595                 600                 605

gcc ggc gat atc atg agc aga gcg ttc atc atc gat cca acg atc agt   1872
Ala Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser
        610                 615                 620

gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa   1920
Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln
    625                 630                 635

ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag   1968
Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu
640                 645                 650                 655

gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg   2016
Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala
                660                 665                 670

gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa   2064
Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu
            675                 680                 685

ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac gac cag gcc   2112
Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala
        690                 695                 700

aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt   2160
Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly
    705                 710                 715
```

ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc 2208
Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val
720 725 730 735

gtc ggg cac gcc cta taa gatatc 2232
Val Gly His Ala Leu
740

<210> 58
<211> 740
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:fusion protein
HTCC#1(184-392)-TbH9-HTCC#1(1-129)

<400> 58
Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Thr
1 5 10 15

Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
20 25 30

Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
35 40 45

Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
50 55 60

Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
65 70 75 80

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
85 90 95

Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
100 105 110

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
115 120 125

Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
130 135 140

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
145 150 155 160

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
165 170 175

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
180 185 190

Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
195 200 205

Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly Ala
210 215 220

Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser
225 230 235 240

Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp
245 250 255

Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr
260 265 270

Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala
275 280 285

Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu
290 295 300

Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr
305 310 315 320

Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu
325 330 335

Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile
340 345 350

Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala
355 360 365

Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu
370 375 380

Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu
385 390 395 400

Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn
405 410 415

Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro
420 425 430

Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr
435 440 445

Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn
450 455 460

Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu
465 470 475 480

Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val
485 490 495

Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser
500 505 510

Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly
515 520 525

Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala
530 535 540

Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser
545 550 555 560

Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu
565 570 575

Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val
580 585 590

Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala
595 600 605

Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala
610 615 620

Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
625 630 635 640

Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu
645 650 655

Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp
660 665 670

Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu
675 680 685

Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn
690 695 700

Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu
705 710 715 720

Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val
725 730 735

Gly His Ala Leu
740

<210> 59
<211> 2365
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
HTCC#1(1-149)-TbH9-HTCC#1(161-392)

<220>
<221> CDS
<222> (4)..(2355)

<400> 59
cat atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat 48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp
1 5 10 15

cca acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga 96
Pro Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly
20 25 30

```
ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa   144
Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu
            35                  40                  45

aaa gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta   192
Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu
        50                  55                  60

ggt tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat   240
Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn
    65                  70                  75

ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc   288
Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile
80                  85                  90                  95

cac gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc   336
His Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly
                100                 105                 110

gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc   384
Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr
            115                 120                 125

tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg   432
Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro
        130                 135                 140

ttt tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt aag ctt atg   480
Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Met
    145                 150                 155

gtg gat ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg tac   528
Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr
160                 165                 170                 175

gcc ggc ccg ggt tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac   576
Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp
                180                 185                 190

agc gtg gcg agt gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg   624
Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val
            195                 200                 205

gtc tgg ggt ctg acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg   672
Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu
        210                 215                 220

atg gtg gcg gcg gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg   720
Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala
    225                 230                 235

ggg cag gcc gag ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc   768
Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala
240                 245                 250                 255

tac gag acg gcg tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag   816
Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu
                260                 265                 270
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aac cgt gct gaa ctg atg att ctg ata gcg acc aac ctc ttg ggg caa    864
Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln
            275                 280                 285

aac acc ccg gcg atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg    912
Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp
        290                 295                 300

gcc caa gac gcc gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg    960
Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr
    305                 310                 315

gcg acg gcg acg ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc   1008
Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser
320                 325                 330                 335

gcg ggt ggg ctc ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac   1056
Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp
                340                 345                 350

acc gcc gcg gcg aac cag ttg atg aac aat gtg ccc cag gcg ctg caa   1104
Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln
            355                 360                 365

cag ctg gcc cag ccc acg cag ggc acc acg cct tct tcc aag ctg ggt   1152
Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly
        370                 375                 380

ggc ctg tgg aag acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg   1200
Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met
    385                 390                 395

gtg tcg atg gcc aac aac cac atg tcg atg acc aac tcg ggt gtg tcg   1248
Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser
400                 405                 410                 415

atg acc aac acc ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg   1296
Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala
                420                 425                 430

gcc gcc cag gcc gtg caa acc gcg gcg caa aac ggg gtc cgg gcg atg   1344
Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met
            435                 440                 445

agc tcg ctg ggc agc tcg ctg ggt tct tcg ggt ctg ggc ggt ggg gtg   1392
Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val
        450                 455                 460

gcc gcc aac ttg ggt cgg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg   1440
Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro
    465                 470                 475

cag gcc tgg gcc gcg gcc aac cag gca gtc acc ccg gcg gcg cgg gcg   1488
Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala
480                 485                 490                 495

ctg ccg ctg acc agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag   1536
Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln
                500                 505                 510
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atg ctg ggc ggg ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt   1584
Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly
            515                 520                 525

ggg ctc agt ggt gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg   1632
Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro
        530                 535                 540

cat tct ccg gca gcc ggc aag ctt act caa ctc ctc aaa ttg ctt gcc   1680
His Ser Pro Ala Ala Gly Lys Leu Thr Gln Leu Leu Lys Leu Leu Ala
    545                 550                 555

aaa ttg gcg gag ttg gtc gcg gcc gcc att gcg gac atc att tcg gat   1728
Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp
560                 565                 570                 575

gtg gcg gac atc atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc   1776
Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile
                580                 585                 590

aca aac gcg ctc aac ggc ctg aaa gag ctt tgg gac aag ctc acg ggg   1824
Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly
            595                 600                 605

tgg gtg acc gga ctg ttc tct cga ggg tgg tcg aac ctg gag tcc ttc   1872
Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe
        610                 615                 620

ttt gcg ggc gtc ccc ggc ttg acc ggc gcg acc agc ggc ttg tcg caa   1920
Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln
    625                 630                 635

gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca tcg tcg ggc ttg   1968
Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu
640                 645                 650                 655

gct cac gcg gat agc ctg gcg agc tca gcc agc ttg ccc gcc ctg gcc   2016
Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala
                660                 665                 670

ggc att ggg ggc ggg tcc ggt ttt ggg ggc ttg ccg agc ctg gct cag   2064
Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln
            675                 680                 685

gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc cga gct gat ggc   2112
Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly
        690                 695                 700

ccg gtc ggc gcc gct gcc gag cag gtc ggc ggg cag tcg cag ctg gtc   2160
Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val
    705                 710                 715

tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta ggc atg ggc ggc   2208
Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly
720                 725                 730                 735

atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg acg aag aag tac   2256
Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr
                740                 745                 750
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tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag cgc gcg cca gtc 2304
Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val
755 760 765

gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta cga aac gtc gtc 2352
Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
770 775 780

taa cggcgaattc 2365

<210> 60
<211> 783
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:fusion protein
HTCC#1(1-149)-TbH9-HTCC#1(161-392)

<400> 60
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro
1 5 10 15

Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile
20 25 30

Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys
35 40 45

Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly
50 55 60

Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe
65 70 75 80

Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His
85 90 95

Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala
100 105 110

Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr
115 120 125

Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe
130 135 140

Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Met Val
145 150 155 160

Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala
165 170 175

Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser
180 185 190

Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val
195 200 205

Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met
210 215 220

Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly
225 230 235 240

Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr
245 250 255

Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn
260 265 270

Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn
275 280 285

Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala
290 295 300

Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala
305 310 315 320

Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala
325 330 335

Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr
340 345 350

Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln
355 360 365

Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly
370 375 380

Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val
385 390 395 400

Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met
405 410 415

Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala
420 425 430

Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser
435 440 445

Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala
450 455 460

Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln
465 470 475 480

Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu
485 490 495

Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met
500 505 510

Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly
515 520 525

Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His
530 535 540

Ser Pro Ala Ala Gly Lys Leu Thr Gln Leu Leu Lys Leu Leu Ala Lys
545 550 555 560

Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
565 570 575

Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr
580 585 590

Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp
595 600 605

Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe
610 615 620

Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val
625 630 635 640

Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala
645 650 655

His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly
660 665 670

Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val
675 680 685

His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro
690 695 700

Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val Ser
705 710 715 720

Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met
725 730 735

His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser
740 745 750

Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu
755 760 765

Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
770 775 780

<210> 61
<211> 2445
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
HTCC#1(184-392)-TbH9-HTCC#1(1-200)

<220>
<221> CDS
<222> (4)..(2439)

<400> 61

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cat atg cat cac cat cac cat cac gat gtg gcg gac atc atc aag ggc   48
    Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly
      1               5                  10                  15

atc ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg   96
Ile Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu
                20                  25                  30

aaa gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct  144
Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser
            35                  40                  45

cga ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg  192
Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu
        50                  55                  60

acc ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg  240
Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala
    65                  70                  75

gcc ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg  288
Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala
80                  85                  90                  95

agc tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt  336
Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly
                100                 105                 110

ttt ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg  384
Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg
            115                 120                 125

cag gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag  432
Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu
        130                 135                 140

cag gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt  480
Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly
    145                 150                 155

atg ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg  528
Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala
160                 165                 170                 175

tcg aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc  576
Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly
                180                 185                 190

act gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg  624
Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly
            195                 200                 205

caa aag gtg ctg gta cga aac gtc gtc gaa ttc atg gtg gat ttc ggg  672
Gln Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly
        210                 215                 220

gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt  720
Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly
    225                 230                 235
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tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt   768
Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser
240                 245                 250                 255

gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg   816
Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu
                260                 265                 270

acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg   864
Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala
            275                 280                 285

gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag   912
Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu
        290                 295                 300

ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg   960
Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala
    305                 310                 315

tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa   1008
Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu
320                 325                 330                 335

ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg   1056
Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala
                340                 345                 350

atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc   1104
Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala
            355                 360                 365

gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg gcg acg gcg acg   1152
Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr
        370                 375                 380

ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc   1200
Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu
    385                 390                 395

ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg   1248
Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala
400                 405                 410                 415

aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag   1296
Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln
                420                 425                 430

ccc acg cag ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag   1344
Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys
            435                 440                 445

acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc   1392
Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala
        450                 455                 460

aac aac cac atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc   1440
Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr
    465                 470                 475
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ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag gcc 1488
Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala
480 485 490 495

gtg caa acc gcg gcg caa aac ggg gtc cgg gcg atg agc tcg ctg ggc 1536
Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly
500 505 510

agc tcg ctg ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg 1584
Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu
515 520 525

ggt cgg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc 1632
Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala
530 535 540

gcg gcc aac cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg ctg acc 1680
Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr
545 550 555

agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg 1728
Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly
560 565 570 575

ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt 1776
Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly
580 585 590

gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca 1824
Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala
595 600 605

gcc ggc gat atc atg agc aga gcg ttc atc atc gat cca acg atc agt 1872
Ala Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser
610 615 620

gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa 1920
Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln
625 630 635

ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag 1968
Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu
640 645 650 655

gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg 2016
Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala
660 665 670

gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa 2064
Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu
675 680 685

ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac gac cag gcc 2112
Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala
690 695 700

aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt 2160
Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly
705 710 715

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ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc   2208
Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val
720                 725                 730                 735

gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg ttt tgc gcg ggc   2256
Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly
                740                 745                 750

gcg atg gcc gta gtg ggc ggc gcg ctt gcc tac ttg gtc gtg aaa acg   2304
Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr
            755                 760                 765

ctg atc aac gcg act caa ctc ctc aaa ttg ctt gcc aaa ttg gcg gag   2352
Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu
        770                 775                 780

ttg gtc gcg gcc gcc att gcg gac atc att tcg gat gtg gcg gac atc   2400
Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile
    785                 790                 795

atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc taa gatatc        2445
Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile
800                 805                 810
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<210> 62
<211> 811
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:fusion protein
HTCC#1(184-392)-TbH9-HTCC#1(1-200)

<400> 62

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Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Ile
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Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
            20                  25                  30

Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
        35                  40                  45

Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
    50                  55                  60

Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
65                  70                  75                  80

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
                85                  90                  95

Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
            100                 105                 110

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
        115                 120                 125

Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
    130                 135                 140
```

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
145 150 155 160

Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
165 170 175

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
180 185 190

Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
195 200 205

Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly Ala
210 215 220

Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser
225 230 235 240

Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp
245 250 255

Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr
260 265 270

Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala
275 280 285

Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu
290 295 300

Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr
305 310 315 320

Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu
325 330 335

Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile
340 345 350

Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala
355 360 365

Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu
370 375 380

Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu
385 390 395 400

Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn
405 410 415

Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro
420 425 430

Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr
435 440 445

Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn
450 455 460

Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu
465 470 475 480

Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val
485 490 495

Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser
500 505 510

Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly
515 520 525

Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala
530 535 540

Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser
545 550 555 560

Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu
565 570 575

Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val
580 585 590

Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala
595 600 605

Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala
610 615 620

Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
625 630 635 640

Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu
645 650 655

Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp
660 665 670

Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu
675 680 685

Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn
690 695 700

Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu
705 710 715 720

Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val
725 730 735

Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala
740 745 750

Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu
755 760 765

Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu
770 775 780

```
Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile
785                 790                 795                 800

Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile
                805                 810
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<210> 63
<211> 1629
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein TbRa12-HTCC#1

<220>
<221> CDS
<222> (4)..(1623)

<400> 63

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cat atg cat cac cat cac cat cac acg gcc gcg tcc gat aac ttc cag   48
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      1               5                  10                  15

ctg tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg   96
Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met
                20                  25                  30

gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat  144
Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His
            35                  40                  45

atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc  192
Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly
        50                  55                  60

aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt  240
Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser
    65                  70                  75

ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg  288
Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro
80                  85                  90                  95

atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc  336
Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro
            100                 105                 110

ggt gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt  384
Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg
        115                 120                 125

aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc cta gta  432
Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Leu Val
    130                 135                 140

cct aga ggt tca atg agc aga gcg ttc atc atc gat cca acg atc agt  480
Pro Arg Gly Ser Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser
145                 150                 155
```

```
gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa   528
Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln
160                 165                 170                 175

ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag   576
Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu
                180                 185                 190

gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg   624
Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala
            195                 200                 205

gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa   672
Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu
        210                 215                 220

ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac gac cag gcc   720
Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala
    225                 230                 235

aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt   768
Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly
240                 245                 250                 255

ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc   816
Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val
                260                 265                 270

gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg ttt tgc gcg ggc   864
Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly
            275                 280                 285

gcg atg gcc gta gtg ggc ggc gcg ctt gcc tac ttg gtc gtg aaa acg   912
Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr
        290                 295                 300

ctg atc aac gcg act caa ctc ctc aaa ttg ctt gcc aaa ttg gcg gag   960
Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu
    305                 310                 315

ttg gtc gcg gcc gcc att gcg gac atc att tcg gat gtg gcg gac atc   1008
Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile
320                 325                 330                 335

atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc   1056
Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu
                340                 345                 350

aac ggc ctg aaa gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga   1104
Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly
            355                 360                 365

ctg ttc tct cga ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc   1152
Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val
        370                 375                 380

ccc ggc ttg acc ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg   1200
Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu
    385                 390                 395
```

```
ttc ggt gcg gcc ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat   1248
Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp
400                 405                 410                 415

agc ctg gcg agc tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc   1296
Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly
                420                 425                 430

ggg tcc ggt ttt ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc   1344
Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala
            435                 440                 445

tca act cgg cag gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc   1392
Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala
        450                 455                 460

gct gcc gag cag gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt   1440
Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly
    465                 470                 475

tcc caa ggt atg ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct   1488
Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser
480                 485                 490                 495

tcg ggg gcg tcg aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg   1536
Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala
                500                 505                 510

gcg gcg ggc act gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg   1584
Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala
            515                 520                 525

ggc ggt ggg caa aag gtg ctg gta cga aac gtc gtc taa gaattc       1629
Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
        530                 535                 540
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<210> 64
<211> 539
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence:fusion protein
TbRa12-HTCC#1

<400> 64

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Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
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Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
            20                  25                  30

Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
        35                  40                  45

Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
    50                  55                  60

Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
65                  70                  75                  80
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Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
85 90 95

Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly
100 105 110

Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
115 120 125

Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Leu Val Pro
130 135 140

Arg Gly Ser Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala
145 150 155 160

Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
165 170 175

Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu
180 185 190

Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp
195 200 205

Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu
210 215 220

Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn
225 230 235 240

Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu
245 250 255

Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val
260 265 270

Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala
275 280 285

Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu
290 295 300

Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu
305 310 315 320

Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile
325 330 335

Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn
340 345 350

Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu
355 360 365

Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro
370 375 380

Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe
385 390 395 400

Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser
405 410 415

Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly
420 425 430

Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser
435 440 445

Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala
450 455 460

Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser
465 470 475 480

Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser
485 490 495

Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala
500 505 510

Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly
515 520 525

Gly Gly Gln Lys Val Leu Val Arg Asn Val Val
530 535

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<210> 91
<211> 8794
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:vector encoding TbF14

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gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg gtgatggttc 240
acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300
ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360
ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg agctgattta 420
acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag gtggcacttt 480
tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt caaatatgta 540
tccgctcatg aattaattct tagaaaaact catcgagcat caaatgaaac tgcaatttat 600
tcatatcagg attatcaata ccatatttttt gaaaaagccg tttctgtaat gaaggagaaa 660
actcaccgag gcagttccat aggatggcaa gatcctggta tcggtctgcg attccgactc 720
gtccaacatc aatacaacct attaatttcc cctcgtcaaa aataaggtta tcaagtgaga 780
aatcaccatg agtgacgact gaatccggtg agaatggcaa aagtttatgc atttctttcc 840
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cgttattcat tcgtgattgc gcctgagcga gacgaaatac gcgatcgctg ttaaaaggac 960

aattacaaac aggaatcgaa tgcaaccggc gcaggaacac tgccagcgca tcaacaatat 1020
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accgaactga gatacctaca gcgtgagcta tgagaaagcg ccacgcttcc cgaagggaga 1920
aaggcggaca ggtatccggt aagcggcagg gtcggaacag gagagcgcac gagggagctt 1980
ccaggggaa acgcctggta tctttatagt cctgtcgggt ttcgccacct ctgacttgag 2040
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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region encoding
His tag

<400> 92
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<210> 93
<211> 8217
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:vector encoding
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gcaggaactc gacgagatct cgacgaatat tcgtcaggcc ggcgtccaat actcgagggc 6600
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cacactggcg gccgctcgag caccaccacc accaccactg agatccggct gctaacaaag 8100
cccgaaagga agctgagttg gctgctgcca ccgctgagca ataactagca taaccccttg 8160
gggcctctaa acgggtcttg aggggttttt tgctgaaagg aggaactata tccggat 8217

<210> 94
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 1 for T-cell epitope mapping

<400> 94
atgagcagag cgttcatcat cgatccaacg atcagtgcca ttgacggctt gtacgacctt 60

<210> 95
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 2 for T-cell epitope
mapping

<400> 95
attgacggct tgtacgacct tctggggatt ggaataccca accaaggggg tatcctttac 60

<210> 96
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 3 for T-cell epitope
mapping

<400> 96
aaccaagggg gtatccttta ctcctcacta gagtacttcg aaaaagccct ggaggagctg 60

<210> 97
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 4 for T-cell epitope
mapping

<400> 97
gaaaaagccc tggaggagct ggcagcagcg tttccgggtg atggctggtt aggttcggcc 60

<210> 98
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 5 for T-cell epitope
mapping

<400> 98
gatggctggt taggttcggc cgcggacaaa tacgccggca aaaaccgcaa ccacgtgaat 60

<210> 99
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 6 for T-cell epitope
mapping

<400> 99
aaaaaccgca accacgtgaa ttttttccag gaactggcag acctcgatcg tcagctcatc 60

<210> 100
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 7 for T-cell epitope
mapping

<400> 100
gacctcgatc gtcagctcat cagcctgatc cacgaccagg ccaacgcggt ccagacgacc 60

<210> 101
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 8 for T-cell epitope
mapping

<400> 101
gccaacgcgg tccagacgac ccgcgacatc ctggagggcg ccaagaaagg tctcgagttc 60

<210> 102
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 9 for T-cell epitope
mapping

<400> 102
gccaagaaag gtctcgagtt cgtgcgcccg gtggctgtgg acctgaccta catcccggtc 60

<210> 103
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 10 for T-cell epitope mapping

<400> 103
gacctgacct acatcccggt cgtcgggcac gccctatcgg ccgccttcca ggcgccgttt 60

<210> 104
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 11 for T-cell epitope mapping

<400> 104
gccgccttcc aggcgccgtt ttgcgcgggc gcgatggccg tagtgggcgg cgcgcttgcc 60

<210> 105
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 12 for T-cell epitope mapping

<400> 105
gtagtgggcg gcgcgcttgc ctacttggtc gtgaaaacgc tgatcaacgc gactcaactc 60

<210> 106
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 13 for T-cell epitope mapping

<400> 106
ctgatcaacg cgactcaact cctcaaattg cttgccaaat tggcggagtt ggtcgcggcc 60

<210> 107
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 14 for T-cell epitope mapping

<400> 107
ttggcggagt tggtcgcggc cgccattgcg gacatcattt cggatgtggc ggacatcatc 60

<210> 108
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 15 for T-cell epitope
mapping

<400> 108
tcggatgtgg cggacatcat caagggcatc ctcggagaag tgtgggagtt catcacaaac 60

<210> 109
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 16 for T-cell epitope
mapping

<400> 109
gtgtgggagt tcatcacaaa cgcgctcaac ggcctgaaag agctttggga caagctcacg 60

<210> 110
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 17 for T-cell epitope
mapping

<400> 110
gagctttggg acaagctcac ggggtgggtg accggactgt tctctcgagg gtggtcgaac 60

<210> 111
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 18 for T-cell epitope
mapping

<400> 111
ttctctcgag ggtggtcgaa cctggagtcc ttctttgcgg gcgtccccgg cttgaccggc 60

<210> 112
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 19 for T-cell epitope mapping

<400> 112
ggcgtccccg gcttgaccgg cgcgaccagc ggcttgtcgc aagtgactgg cttgttcggt 60

<210> 113
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 20 for T-cell epitope mapping

<400> 113
caagtgactg gcttgttcgg tgcggccggt ctgtccgcat cgtcgggctt ggctcacgcg 60

<210> 114
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 21 for T-cell epitope mapping

<400> 114
tcgtcgggct tggctcacgc ggatagcctg gcgagctcag ccagcttgcc cgccctggcc 60

<210> 115
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 22 for T-cell epitope mapping

<400> 115
gccagcttgc ccgccctggc cggcattggg ggcgggtccg gttttggggg cttgccgagc 60

<210> 116
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 23 for T-cell epitope mapping

<400> 116
ggttttgggg gcttgccgag cctggctcag gtccatgccg cctcaactcg gcaggcgcta 60

<210> 117
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 24 for T-cell epitope mapping

<400> 117
gcctcaactc ggcaggcgct acggccccga gctgatggcc cggtcggcgc cgctgccgag 60

<210> 118
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 25 for T-cell epitope mapping

<400> 118
ccggtcggcg ccgctgccga gcaggtcggc gggcagtcgc agctggtctc cgcgcagggt 60

<210> 119
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 26 for T-cell epitope mapping

<400> 119
cagctggtct ccgcgcaggg ttcccaaggt atgggcggac ccgtaggcat gggcggc 57

<210> 120
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid sequence of HTCC#1 peptide 27 for T-cell epitope mapping

<400> 120
cccgtaggca tgggcggcat gcacccctct tcgggggcgt cgaaagggac gacgacgaag 60

<210> 121
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 28 for T-cell epitope
mapping

<400> 121
tcgaaaggga cgacgacgaa gaagtactcg gaaggcgcgg cggcgggcac tgaagacgcc 60

<210> 122
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 29 for T-cell epitope
mapping

<400> 122
gcggcgggca ctgaagacgc cgagcgcgcg ccagtcgaag ctgacgcggg cggtgggcaa 60

<210> 123
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nucleic acid
sequence of HTCC#1 peptide 30 for T-cell epitope
mapping

<400> 123
cgcgcgccag tcgaagctga cgcgggcggt gggcaaaagg tgctggtacg aaacgtcgtc 60

<210> 124
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
1 for T-cell epitope mapping

<400> 124
Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1 5 10 15

Leu Tyr Asp Leu
20

<210> 125
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
2 for T-cell epitope mapping

<400> 125
Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly
1 5 10 15

Gly Ile Leu Tyr
20

<210> 126
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
3 for T-cell epitope mapping

<400> 126
Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala
1 5 10 15

Leu Glu Glu Leu
20

<210> 127
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
4 for T-cell epitope mapping

<400> 127
Glu Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp
1 5 10 15

Leu Gly Ser Ala
20

<210> 128
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
5 for T-cell epitope mapping

<400> 128
Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg
1 5 10 15

Asn His Val Asn
20

<210> 129
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
6 for T-cell epitope mapping

<400> 129
Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu Asp
1 5 10 15

Arg Gln Leu Ile
20

<210> 130
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
7 for T-cell epitope mapping

<400> 130
Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala
1 5 10 15

Val Gln Thr Thr
20

<210> 131
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
8 for T-cell epitope mapping

<400> 131
Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys
1 5 10 15

Gly Leu Glu Phe
20

<210> 132
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
9 for T-cell epitope mapping

<400> 132
Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr
1 5 10 15

Tyr Ile Pro Val
20

<210> 133
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
10 for T-cell epitope mapping

<400> 133
Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe
1 5 10 15

Gln Ala Pro Phe
20

<210> 134
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
11 for T-cell epitope mapping

<400> 134
Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly
1 5 10 15

Gly Ala Leu Ala
20

<210> 135
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
12 for T-cell epitope mapping

<400> 135
Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn
1 5 10 15

Ala Thr Gln Leu
20

<210> 136
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
13 for T-cell epitope mapping

<400> 136
Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu
1 5 10 15

Leu Val Ala Ala
20

<210> 137
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
14 for T-cell epitope mapping

<400> 137
Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val
1 5 10 15

Ala Asp Ile Ile
20

<210> 138
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
15 for T-cell epitope mapping

<400> 138
Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu
1 5 10 15

Phe Ile Thr Asn
20

<210> 139
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
16 for T-cell epitope mapping

<400> 139
Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp
1 5 10 15

Asp Lys Leu Thr
20

<210> 140
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
17 for T-cell epitope mapping

<400> 140
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
1 5 10 15

Gly Trp Ser Asn
20

<210> 141
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
18 for T-cell epitope mapping

<400> 141
Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro
1 5 10 15

Gly Leu Thr Gly
20

<210> 142
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
19 for T-cell epitope mapping

<400> 142
Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr
1 5 10 15

Gly Leu Phe Gly
20

<210> 143
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
20 for T-cell epitope mapping

<400> 143
Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly
1 5 10 15

Leu Ala His Ala
20

<210> 144
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
21 for T-cell epitope mapping

<400> 144
Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu
1 5 10 15

Pro Ala Leu Ala
20

<210> 145
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
22 for T-cell epitope mapping

<400> 145
Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly
1 5 10 15

Gly Leu Pro Ser
20

<210> 146
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
23 for T-cell epitope mapping

<400> 146
Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr
1 5 10 15

Arg Gln Ala Leu
20

<210> 147
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
24 for T-cell epitope mapping

<400> 147
Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly
1 5 10 15

Ala Ala Ala Glu
20

<210> 148
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
25 for T-cell epitope mapping

<400> 148
Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val
1 5 10 15

Ser Ala Gln Gly
20

<210> 149
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
26 for T-cell epitope mapping

<400> 149
Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly
1 5 10 15

Met Gly Gly

<210> 150
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
27 for T-cell epitope mapping

<400> 150
Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly
1 5 10 15

Thr Thr Thr Lys
20

<210> 151
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
28 for T-cell epitope mapping

<400> 151
Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly
1 5 10 15

Thr Glu Asp Ala
20

<210> 152
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
29 for T-cell epitope mapping

<400> 152
Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala
1 5 10 15

Gly Gly Gly Gln
20

<210> 153
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HTCC#1 peptide
30 for T-cell epitope mapping

<400> 153
Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val
1 5 10 15

Arg Asn Val Val
20

<210> 154
<211> 84
<212> PRT
<213> Mycobacterium tuberculosis

<220>
<223> secreted form of DPPD

<400> 154
Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro
1 5 10 15

Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys
20 25 30

Tyr Pro Asp Gly Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr
35 40 45

Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro
50 55 60

Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln
65 70 75 80

Pro Asn Ala Pro

<210> 155
<211> 2836
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<223> Mtb9.9A (MTI-A)

<400> 155
gttgattccg ttcgcggcgc cgccgaagac caccaactcc gctggggtgg tcgcacaggc 60
ggttgcgtcg gtcagctggc cgaatcccaa tgattggtgg ctcngtgcgg ttgctgggct 120
cgattacccc cacggaaagg acgacgatcg ttcgtttgct cggtcagtcg tacttggcga 180
cgggcatggc gcggtttctt acctcgatcg cacagcagct gaccttcggc ccaggggca 240
caacggctgg ctccggcgga gcctggtacc caacgccaca attcgccggc ctgggtgcag 300
gcccggcggt gtcggcgagt ttggcgcggg cggagccggt cgggaggttg tcggtgccgc 360
caagttgggc cgtcgcggct ccggccttcg cggagaagcc tgaggcgggc acgccgatgt 420
ccgtcatcgg cgaagcgtcc agctgcggtc agggaggcct gcttcgaggc ataccgctgg 480

cgagagcggg gcggcgtaca ggcgccttcg ctcaccgata cgggttccgc cacagcgtga 540
ttacccggtc tccgtcggcg ggatagcttt cgatccggtc tgcgcggccg ccggaaatgc 600
tgcagatagc gatcgaccgc gccggtcggt aaacgccgca cacggcacta tcaatgcgca 660
cggcgggcgt tgatgccaaa ttgaccgtcc cgacggggct ttatctgcgg caagatttca 720
tccccagccc ggtcggtggg ccgataaata cgctggtcag cgcgactctt ccggctgaat 780
tcgatgctct gggcgcccgc tcgacgccga gtatctcgag tgggccgcaa acccggtcaa 840
acgctgttac tgtggcgtta ccacaggtga atttgcggtg ccaactggtg aacacttgcg 900
aacgggtggc atcgaaatca acttgttgcg ttgcagtgat ctactctctt gcagagagcc 960
gttgctggga ttaattggga gaggaagaca gcatgtcgtt cgtgaccaca cagccggaag 1020
ccctggcagc tgcggcggcg aacctacagg gtattggcac gacaatgaac gcccagaacg 1080
cggccgcggc tgctccaacc accggagtag tgcccgcagc cgccgatgaa gtatcagcgc 1140
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ccatgggttc ttcccg 2836

<210> 156
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 156
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala
1 5 10 15

<210> 157
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 157
Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
1 5 10 15

<210> 158
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 158
Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
1 5 10 15

<210> 159
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 159
Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala
1 5 10 15

<210> 160
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 160
Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val
1 5 10 15

<210> 161
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 161
Ala Glu His Gln Ala Ile Val Arg Asp Val Leu Ala Ala Gly Asp
1 5 10 15

<210> 162
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 162
Ile Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala
1 5 10 15

<210> 163
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 163
Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln
1 5 10 15

<210> 164
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 164
Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr
1 5 10 15

<210> 165
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 165
Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn
1 5 10 15

<210> 166
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 166
Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu
1 5 10 15

Gln Ala

<210> 167
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 167
Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln
1 5 10 15

<210> 168
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 168
Ile Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala
1 5 10 15

<210> 169
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 169
Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala
1 5 10 15

<210> 170
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 170
Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala
1 5 10 15

<210> 171
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
ORF peptide

<400> 171
Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
1 5 10 15

<210> 172
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 172
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln
1 5 10 15

<210> 173
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF
peptide

<400> 173
Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
1 5 10 15

<210> 174
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 174
Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
1 5 10 15

<210> 175
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 175
Ser Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly
1 5 10 15

<210> 176
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 176
Lys Ala Gly Leu Met His Thr Ile Gly Gln Ala Glu Gln Ala
1 5 10

<210> 177
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 177
Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala Met Ser Ala Gln
1 5 10 15

<210> 178
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 178
Gln Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly
1 5 10 15

<210> 179
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 179
Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala
1 5 10 15

<210> 180
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 180
Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His
1 5 10 15

<210> 181
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 181
Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala
1 5 10 15

<210> 182
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 182
Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys Val
1 5 10 15

<210> 183
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 183
Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Leu Leu Asp
1 5 10 15

<210> 184
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 184
Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn
1 5 10 15

<210> 185
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 185
Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
1 5 10 15

<210> 186
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Mtb9.8 ORF peptide

<400> 186
Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala
1 5 10 15

Asp Ala

<210> 187
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR amplification primer PDM-294

<400> 187
cgtaatcacg tgcagaagta cggcggatc 29

<210> 188
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR amplification primer PDM-295

<400> 188
ccgactagaa ttcactattg acaggcccat c 31

<210> 189
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR amplification primer PDM-268

<400> 189
ctaagtagta ctgatcgcgt gtcggtgggc 30

<210> 190
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR amplification primer PDM-296

<400> 190
catcgatagg cctggccgca tcgtcacc 28

<210> 191
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR amplification primer PDM-157

<400> 191
ctagttagta ctcagtcgca gaccgtg 27

<210> 192
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR amplification primer PDM-160

<400> 192
gcagtgacga attcacttcg actcc 25

<210> 193
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR amplification primer PDM-69

<400> 193
ggatccagcg ctgagatgaa gaccgatgcc gct 33

<210> 194
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR amplification primer PDM-83

<400> 194
ggatatctgc agaattcagg tttaaagccc atttgcga 38

<210> 195
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR amplification primer PDM-192

<400> 195
tgtggctcga aaccaccgag cggttc 26

<210> 196
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer PDM-60

<400> 196
gagagaattc tcagaagccc atttgcgagg aca 33

<210> 197
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
oligonucleotide 5' primer

<400> 197
caattacata tgcatcacca tcaccatcac atgagcagag cgttcatcat c 51

<210> 198
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
oligonucleotide 3' primer

<400> 198
catggaattc gccgttagac gacgtttcgt a 31

<210> 199
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification oligonucleotide 5' primer

<400> 199
caattacata tgcatcacca tcaccatcac acggccgcgt ccgataactt c 51

<210> 200
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification oligonucleotide 3' primer

<400> 200
ctaatcgaat tcggccgggg gtccctcggc caa 33

<210> 201
<211> 1179
<212> DNA
<213> Mycobacterium tuberculosis

<220>
<221> CDS
<222> (1)..(1179)
<223> HTCC#1

<400> 201

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Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
  1               5                  10                  15

ttg tac gac ctt ctg ggg att gga ata ccc aac caa ggg ggt atc ctt   96
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
             20                  25                  30

tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag gag ctg gca gca   144
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
         35                  40                  45

gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg gac aaa tac gcc   192
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
     50                  55                  60

ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa ctg gca gac ctc   240
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
 65                  70                  75                  80

gat cgt cag ctc atc agc ctg atc cac gac cag gcc aac gcg gtc cag   288
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
                 85                  90                  95

acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt ctc gag ttc gtg   336
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
            100                 105                 110

cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc gtc ggg cac gcc   384
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
        115                 120                 125

cta tcg gcc gcc ttc cag gcg ccg ttt tgc gcg ggc gcg atg gcc gta   432
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
    130                 135                 140

gtg ggc ggc gcg ctt gcc tac ttg gtc gtg aaa acg ctg atc aac gcg   480
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145                 150                 155                 160

act caa ctc ctc aaa ttg ctt gcc aaa ttg gcg gag ttg gtc gcg gcc   528
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
                165                 170                 175

gcc att gcg gac atc att tcg gat gtg gcg gac atc atc aag ggc atc   576
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile
            180                 185                 190
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ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa   624
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
        195                 200                 205

gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga   672
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
    210                 215                 220

ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc   720
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225                 230                 235                 240

ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc   768
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
                245                 250                 255

ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc   816
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
            260                 265                 270

tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt   864
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
        275                 280                 285

ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg cag   912
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
    290                 295                 300

gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag   960
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
305                 310                 315                 320

gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg  1008
Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
                325                 330                 335

ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg  1056
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
            340                 345                 350

aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act  1104
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
        355                 360                 365

gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa  1152
Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
    370                 375                 380

aag gtg ctg gta cga aac gtc gtc taa                             1179
Lys Val Leu Val Arg Asn Val Val
385                 390
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<210> 202
<211> 392
<212> PRT
<213> Mycobacterium tuberculosis

<400> 202

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Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
  1               5                  10                  15
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Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
            20                  25                  30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
        35                  40                  45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
    50                  55                  60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65                  70                  75                  80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
                85                  90                  95

Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
            100                 105                 110

Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
        115                 120                 125

Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
    130                 135                 140

Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145                 150                 155                 160

Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
                165                 170                 175

Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile
            180                 185                 190

Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
        195                 200                 205

Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
    210                 215                 220

Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225                 230                 235                 240

Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
                245                 250                 255

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
            260                 265                 270

Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
        275                 280                 285

Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
    290                 295                 300

Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
305                 310                 315                 320

Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
                325                 330                 335
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Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
340 345 350

Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
355 360 365

Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln
370 375 380

Lys Val Leu Val Arg Asn Val Val
385 390